PP01598 / 200130.512

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4	29372	RTA00002712F.a.06.1.P.Seq	F	M00023282A:C02	CH04MAL
5	455003	RTA00002694F.b.02.1.P.Seq	F	M00043419D:A10	CH20COHLV
6	380625	RTA00002684F.d.03.2.P.Seq	F	M00040118D:G10	CH09LNL
7	450959	RTA00002691F.b.05.3.P.Seq	F	M00043306D:B07	CH17COHLV
8	397851	RTA00002680F.b.04.1.P.Seq	F	M00039775A:A09	CH09LNL
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16	375772	RTA00002681F.p.01.2.P.Seq	F	M00039909C:G05	CH09LNL
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18	376546	RTA00002677F.d.07.2.P.Seq	F	M00039345C:C12	CH09LNL
19	430041	RTA00002667F.f.17.1.P.Seq	F	M00032790B:A07	CH08LNH
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22	376802	RTA00002677F.c.18.2.P.Seq	F	M00039344B:G07	CH09LNL
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26	380668	RTA00002670F.p.11.1.P.Seq	F	M00033581C:H10	CH09LNL
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33	374846	RTA00002677F.k.19.2.P.Seq	F	M00039412D:G06	CH09LNL
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59	375666	RTA00002677F.n.16.2.P.Seq	F	M00039422D:F04	CH09LNL
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92	377086	RTA00002676F.p.07.1.P.Seq	F	M00039328D:D07	CH09LNL
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144	379114	RTA00002681F.o.01.2.P.Seq	F	M00039903C:F03	CH09LNL
145	19609	RTA00002709F.c.05.1.P.Seq	F	M00005457C:A03	CH02COH
146	21685	RTA00002709F.e.23.1.P.Seq	F	M00006581D:F08	CH02COH
147	380085	RTA00002682F.i.10.1.P.Seq	F	M00039987A:F09	CH09LNL
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537	17430	RTA00002710F.i.11.1.P.Seq	F	M00022365D:A03	CH03MAH
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653	428508	RTA00002666F.d.01.1.P.Seq	F	M00032545B:H09	CH08LNH
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671	146260	RTA00002663F.d.17.1.P.Seq	F	M00022099B:D06	CH03MAH
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708	378667	RTA00002681F.b.11.2.P.Seq	F	M00039847A:F06	CH09LNL
709	380454	RTA00002673F.j.16.1.P.Seq	F	M00039084D:D07	CH09LNL
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718	98471	RTA00002663F.j.21.1.P.Seq	F	M00022670D:H11	CH03MAH
719	125365	RTA00002668F.j.07.1.P.Seq	F	M00033019B:E10	CH08LNH
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724	230479	RTA00002664F.c.16.2.P.Seq	F	M00026915B:C06	CH04MAL
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757	431370	RTA00002669F.m.04.3.P.Seq	F	M00033288B:D12	CH08LNH
758	380500	RTA00002670F.p.19.1.P.Seq	F	M00033583B:E06	CH09LNL
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760	191690	RTA00002673F.m.19.1.P.Seq	F	M00039107C:E04	CH09LNL
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1029	373875	RTA00002674F.c.05.1.P.Seq	F	M00039124C:H02	CH09LNL
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1040	406092	RTA00002685F.k.11.1.P.Seq	F	M00039584C:C11	CH12EDT
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1043	401828	RTA00002686F.j.14.1.P.Seq	F	M00040232D:B07	CH13EDT
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1049	402952	RTA00002686F.g.14.1.P.Seq	F	M00040181D:H10	CH13EDT
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1074	400517	RTA00002687F.k.15.1.P.Seq	F	M00040320D:F02	CH14EDT
1075	456636	RTA00002694F.e.05.1.P.Seq	F	M00043632D:F09	CH20COHLV
1076	400101	RTA00002685F.o.04.1.P.Seq	F	M00039625B:G08	CH12EDT
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1087	413643	RTA00002685F.n.05.2.P.Seq	F	M00039604D:G03	CH12EDT
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1089	376511	RTA00002674F.h.04.1.P.Seq	F	M00039140A:B08	CH09LNL
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1132	401437	RTA00002685F.c.18.1.P.Seq	F	M00039377D:E12	CH12EDT
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1139	449832	RTA00002691F.e.13.1.P.Seq	F	M00043393A:B08	CH17COHLV
1140	379004	RTA00002683F.n.09.2.P.Seq	F	M00040093B:C02	CH09LNL
1141	455211	RTA00002694F.b.07.1.P.Seq	F	M00043430B:C02	CH20COHLV
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1143	376279	RTA00002680F.d.10.2.P.Seq	F	M00039785D:G05	CH09LNL
1144	374373	RTA00002681F.n.21.1.P.Seq	F	M00039903A:H07	CH09LNL
1145	97668	RTA00002686F.d.19.1.P.Seq	F	M00040145D:D03	CH13EDT
1146	400407	RTA00002685F.a.05.2.P.Seq	F	M00039184A:D03	CH12EDT
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1152	401471	RTA00002685F.o.10.1.P.Seq	F	M00039629B:F01	CH12EDT
1153	404362	RTA00002687F.o.06.2.P.Seq	F	M00040342B:D12	CH14EDT
1154	373641	RTA00002677F.i.09.2.P.Seq	F	M00039403A:G12	CH09LNL
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1217	400147	RTA00002685F.g.10.2.P.Seq	F	M00039515A:A06	CH12EDT
1218	401655	RTA00002685F.c.22.2.P.Seq	F	M00039378D:H07	CH12EDT
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1220	403121	RTA00002688F.a.01.2.P.Seq	F	M00040366A:B01	CH14EDT
1221	451718	RTA00002692F.e.24.1.P.Seq	F	M00043044B:A12	CH18CON
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1227	376236	RTA00002685F.l.24.2.P.Seq	F	M00039595C:E05	CH12EDT
1228	422357	RTA00002688F.c.21.1.P.Seq	F	M00040385C:D02	CH14EDT
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1230	403693	RTA00002687F.j.23.1.P.Seq	F	M00040317D:F02	CH14EDT
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1232	401515	RTA00002685F.o.02.2.P.Seq	F	M00039624B:F12	CH12EDT
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1259	451013	RTA00002691F.f.08.2.P.Seq	F	M00043409B:B03	CH17COHLV
1260	453011	RTA00002692F.f.10.1.P.Seq	F	M00043066B:H11	CH18CON
1261	380462	RTA00002670F.n.24.2.P.Seq	F	M00033570B:E06	CH09LNL
1262	379602	RTA00002681F.c.21.2.P.Seq	F	M00039855C:F01	CH09LNL
1263	403896	RTA00002687F.a.04.1.P.Seq	F	M00039746C:H05	CH14EDT
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1266	451379	RTA00002691F.b.12.2.P.Seq	F	M00043312C:E08	CH17COHLV
1267	456624	RTA00002694F.e.02.1.P.Seq	F	M00043616B:F02	CH20COHLV
1268	375483	RTA00002686F.n.14.1.P.Seq	F	M00040274A:D07	CH13EDT
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1272	401381	RTA00002685F.o.08.1.P.Seq	F	M00039626D:F04	CH12EDT
1273	428491	RTA00002666F.c.05.1.P.Seq	F	M00032535D:H01	CH08LNH
1274	54656	RTA00002661F.i.22.2.P.Seq	F	M00004372B:F07	CH01COH
1275	379183	RTA00002679F.i.17.1.P.Seq	F	M00039688C:G06	CH09LNL
1276	25594	RTA00002711F.f.07.1.P.Seq	F	M00022968B:E02	CH03MAH
1277	403355	RTA00002687F.d.11.1.P.Seq	F	M00039948D:D11	CH14EDT
1278	16789	RTA00002709F.b.09.2.P.Seq	F	M00005382B:F08	CH02COH
1279	23292	RTA00002708F.c.02.1.P.Seq	F	M00003750D:E06	CH01COH
1280	373982	RTA00002673F.b.24.2.P.Seq	F	M00039058A:A04	CH09LNL
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1282	449911	RTA00002691F.e.02.2.P.Seq	F	M00043384B:B02	CH17COHLV
1283	450633	RTA00002691F.f.02.2.P.Seq	F	M00043405C:G12	CH17COHLV
1284	23939	RTA00002713F.j.14.1.P.Seq	F	M00027486A:F06	CH04MAL
1285	450633	RTA00002691F.f.02.1.P.Seq	F	M00043405C:G12	CH17COHLV
1286	379122	RTA00002672F.n.14.1.P.Seq	F	M00039039B:F09	CH09LNL
1287	449429	RTA00002690F.a.16.3.P.Seq	F	M00042437A:D04	CH16COP
1288	430578	RTA00002668F.g.18.1.P.Seq	F	M00032984C:G05	CH08LNH
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1291	401266	RTA00002685F.i.11.2.P.Seq	F	M00039535D:D10	CH12EDT
1292	377949	RTA00002674F.p.04.1.P.Seq	F	M00039200A:C10	CH09LNL
1293	12926	RTA00002710F.e.21.1.P.Seq	F	M00022005C:C06	CH03MAH
1294	378242	RTA00002679F.c.20.2.P.Seq	F	M00039664D:G07	CH09LNL
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1296	453101	RTA00002693F.c.16.2.P.Seq	F	M00043143B:A10	CH19COP
1297	377592	RTA00002677F.l.12.2.P.Seq	F	M00039415D:E01	CH09LNL
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1306	375226	RTA00002677F.m.08.2.P.Seq	F	M00039417C:A01	CH09LNL
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1310	455579	RTA00002694F.a.10.1.P.Seq	F	M00042596B:F06	CH20COHLV
1311	13406	RTA00002709F.l.14.1.P.Seq	F	M00007124D:H10	CH02COH
1312	378364	RTA00002674F.o.17.1.P.Seq	F	M00039196D:A07	CH09LNL
1313	373788	RTA00002671F.c.16.2.P.Seq	F	M00038259A:G08	CH09LNL
1314	403548	RTA00002688F.a.10.2.P.Seq	F	M00040368D:E09	CH14EDT
1315	22425	RTA00002709F.c.08.2.P.Seq	F	M00005498A:H06	CH02COH
1316	452238	RTA00002692F.c.21.2.P.Seq	F	M00042998A:G04	CH18CON

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1319	450196	RTA00002691F.c.19.3.P.Seq	F	M00043359B:D10	CH17COHLV
1320	26017	RTA00002709F.d.04.1.P.Seq	F	M00005601D:D08	CH02COH
1321	380355	RTA00002670F.o.06.1.P.Seq	F	M00033570C:C10	CH09LNL
1322	25232	RTA00002710F.n.22.1.P.Seq	F	M00022667D:B02	CH03MAH
1323	378952	RTA00002683F.h.11.1.P.Seq	F	M00040070B:B07	CH09LNL
1324	404487	RTA00002687F.c.13.2.P.Seq	F	M00039943B:F10	CH14EDT
1325	48482	RTA00002712F.p.06.1.P.Seq	F	M00027159D:F03	CH04MAL
1326	373705	RTA00002673F.a.13.1.P.Seq	F	M00039052C:F07	CH09LNL
1327	373705	RTA00002673F.a.13.2.P.Seq	F	M00039052C:F07	CH09LNL
1328	21162	RTA00002709F.c.03.1.P.Seq	F	M00005449B:D01	CH02COH
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1331	401013	RTA00002685F.o.16.2.P.Seq	F	M00039641A:A05	CH12EDT
1332	404449	RTA00002687F.c.04.2.P.Seq	F	M00039770C:E04	CH14EDT
1333	429672	RTA00002668F.b.10.1.P.Seq	F	M00032909A:B06	CH08LNH
1334	48541	RTA00002712F.i.07.1.P.Seq	F	M00026922C:B02	CH04MAL
1335	378424	RTA00002681F.a.03.2.P.Seq	F	M00039839B:B01	CH09LNL
1336	49540	RTA00002712F.d.24.1.P.Seq	F	M00023399C:E10	CH04MAL
1337	379170	RTA00002672F.i.21.1.P.Seq	F	M00039016D:G06	CH09LNL
1338	179540	RTA00002683F.o.20.2.P.Seq	F	M00040100C:E05	CH09LNL
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1340	449832	RTA00002691F.e.13.2.P.Seq	F	M00043393A:B08	CH17COHLV
1341	380119	RTA00002670F.m.20.2.P.Seq	F	M00033560D:G07	CH09LNL
1342	153094	RTA00002714F.a.12.1.P.Seq	F	M00027743A:C03	CH04MAL
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1352	428063	RTA00002666F.l.05.1.P.Seq	F	M00032638C:G08	CH08LNH
1353	374722	RTA00002676F.j.19.3.P.Seq	F	M00039310A:C07	CH09LNL
1354	428407	RTA00002665F.p.12.1.P.Seq	F	M00032510D:F12	CH08LNH
1355	378000	RTA00002681F.j.16.1.P.Seq	F	M00039887D:C04	CH09LNL
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1360	431346	RTA00002669F.g.24.2.P.Seq	F	M00033218A:C04	CH08LNH
1361	377206	RTA00002682F.m.14.1.P.Seq	F	M00040015C:F08	CH09LNL
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1367	379011	RTA00002681F.n.23.1.P.Seq	F	M00039903C:D01	CH09LNL
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1388	403796	RTA00002687F.h.17.1.P.Seq	F	M00040293D:G04	CH14EDT
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1396	134877	RTA00002662F.d.05.2.P.Seq	F	M00007026B:H09	CH02COH
1397	372811	RTA00002670F.c.12.2.P.Seq	F	M00033347C:F02	CH09LNL
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1414	375589	RTA00002680F.f.06.1.P.Seq	F	M00039794A:E04	CH09LNL
1415	375789	RTA00002674F.a.16.1.P.Seq	F	M00039120C:H03	CH09LNL
1416	456227	RTA00002694F.c.16.1.P.Seq	F	M00043465C:C09	CH20COHLV
1417	455852	RTA00002694F.a.02.1.P.Seq	F	M00042592A:H10	CH20COHLV
1418	25169	RTA00002710F.m.05.1.P.Seq	F	M00022579C:C11	CH03MAH
1419	376524	RTA00002678F.h.23.2.P.Seq	F	M00039477A:B03	CH09LNL
1420	449562	RTA00002690F.b.13.2.P.Seq	F	M00042515C:F08	CH16COP
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1461	401013	RTA00002685F.o.16.1.P.Seq	F	M00039641A:A05	CH12EDT
1462	74344	RTA00002661F.f.10.1.P.Seq	F	M00003902A:C03	CH01COH
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1465	379560	RTA00002682F.g.18.1.P.Seq	F	M00039981A:E08	CH09LNL
1466	122669	RTA00002712F.f.22.1.P.Seq	F	M00026857D:G12	CH04MAL
1467	373319	RTA00002671F.c.17.2.P.Seq	F	M00038259B:A02	CH09LNL
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1474	446404	RTA00002689F.e.02.3.P.Seq	F	M00042887C:D07	CH15CON
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1482	449080	RTA00002690F.a.04.2.P.Seq	F	M00042347D:H11	CH16COP
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1503	394113	RTA00002665F.d.15.3.P.Seq	F	M00028314D:F05	CH08LNH
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1507	455142	RTA00002694F.b.08.1.P.Seq	F	M00043431D:B08	CH20COHLV
1508	117060	RTA00002679F.i.01.1.P.Seq	F	M00039686C:C05	CH09LNL
1509	447859	RTA00002689F.d.13.1.P.Seq	F	M00042737C:H04	CH15CON
1510	452572	RTA00002692F.e.16.1.P.Seq	F	M00043034D:C01	CH18CON
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1514	404084	RTA00002688F.d.16.2.P.Seq	F	M00040392B:H01	CH14EDT
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1516	229665	RTA00002664F.c.08.2.P.Seq	F	M00026885A:H09	CH04MAL
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1524	230842	RTA00002665F.n.15.1.P.Seq	F	M00032492A:C01	CH08LNH
1525	450149	RTA00002692F.a.20.2.P.Seq	F	M00042630A:C05	CH18CON
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1531	376897	RTA00002674F.l.20.1.P.Seq	F	M00039167B:H09	CH09LNL
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1597	449524	RTA00002690F.a.11.3.P.Seq	F	M00042432D:E02	CH16COP
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1599	447583	RTA00002690F.b.20.3.P.Seq	F	M00042756B:F11	CH16COP
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1601	450609	RTA00002691F.a.13.3.P.Seq	F	M00042453B:G09	CH17COHLV
1602	447528	RTA00002689F.c.10.1.P.Seq	F	M00042698D:D10	CH15CON
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1606	449538	RTA00002690F.b.17.3.P.Seq	F	M00042752A:E11	CH16COP
1607	411128	RTA00002720F.a.02.4.P.Seq	F	M00043022A:E12	CH18CON
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1612	38403	RTA00002693F.c.11.2.P.Seq	F	M00043138D:B11	CH19COP
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1615	449285	RTA00002690F.d.24.3.P.Seq	F	M00042823C:C02	CH16COP
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1623	377284	RTA00002683F.g.06.1.P.Seq	F	M00040060C:H10	CH09LNL
1624	449496	RTA00002690F.e.06.1.P.Seq	F	M00042830B:E02	CH16COP
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1631	376897	RTA00002674F.l.20.2.P.Seq	F	M00039167B:H09	CH09LNL
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1638	449285	RTA00002690F.e.01.2.P.Seq	F	M00042823C:C02	CH16COP
1639	377284	RTA00002683F.g.06.2.P.Seq	F	M00040060C:H10	CH09LNL
1640	377605	RTA00002683F.m.02.2.P.Seq	F	M00040089B:E04	CH09LNL
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1646	447069	RTA00002689F.b.15.1.P.Seq	F	M00042567B:H10	CH15CON
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1648	32699	RTA00002713F.i.24.1.P.Seq	F	M00027475B:E10	CH04MAL
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1664	227947	RTA00002684F.h.08.2.P.Seq	F	M00040307C:F10	CH09LNL
1665	429182	RTA00002666F.g.23.1.P.Seq	F	M00032592A:H11	CH08LNH
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1667	373614	RTA00002671F.m.06.2.P.Seq	F	M00038329A:E08	CH09LNL
1668	453281	RTA00002693F.a.03.1.P.Seq	F	M00042611D:B12	CH19COP
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1674	430566	RTA00002666F.d.12.1.P.Seq	F	M00032551B:G05	CH08LNH
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1677	447737	RTA00002689F.c.15.1.P.Seq	F	M00042704A:F09	CH15CON
1678	450261	RTA00002691F.e.09.1.P.Seq	F	M00043389D:D07	CH17COHLV
1679	453281	RTA00002693F.a.03.2.P.Seq	F	M00042611D:B12	CH19COP
1680	378994	RTA00002670F.f.03.1.P.Seq	F	M00033376A:C12	CH09LNL
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1682	379097	RTA00002683F.o.14.2.P.Seq	F	M00040098D:E04	CH09LNL
1683	426895	RTA00002691F.c.16.3.P.Seq	F	M00043352D:B05	CH17COHLV
1684	159000	RTA00002712F.i.22.1.P.Seq	F	M00026944B:E03	CH04MAL
1685	377088	RTA00002682F.m.06.1.P.Seq	F	M00040014D:D10	CH09LNL
1686	20990	RTA00002670F.f.13.2.P.Seq	F	M00033377D:A05	CH09LNL
1687	379131	RTA00002682F.p.04.1.P.Seq	F	M00040026B:F06	CH09LNL
1688	179262	RTA00002712F.g.21.1.P.Seq	F	M00026878A:F05	CH04MAL
1689	378947	RTA00002683F.o.12.1.P.Seq	F	M00040098C:B01	CH09LNL
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1693	380354	RTA00002670F.n.23.2.P.Seq	F	M00033570B:C08	CH09LNL
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1697	379896	RTA00002680F.a.24.2.P.Seq	F	M00039774C:C09	CH09LNL
1698	377679	RTA00002678F.a.09.2.P.Seq	F	M00039431B:F04	CH09LNL

1699	254091	RTA00002677F.a.13.2.P.Seq	F	M00039335A:E08	CH09LNL
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1704	453877	RTA00002693F.d.16.2.P.Seq	F	M00043165B:G01	CH19COP
1705	379808	RTA00002680F.j.16.1.P.Seq	F	M00039813B:B01	CH09LNL
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1708	24045	RTA00002709F.l.17.1.P.Seq	F	M00007136A:A03	CH02COH
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1713	456127	RTA00002694F.c.04.1.P.Seq	F	M00043453B:B09	CH20COHLV
1714	374680	RTA00002676F.c.14.2.P.Seq	F	M00039279C:B08	CH09LNL
1715	429089	RTA00002666F.n.14.1.P.Seq	F	M00032668D:G12	CH08LNH
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1721	16774	RTA00002709F.b.02.1.P.Seq	F	M00005352C:A02	CH02COH
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1724	455850	RTA00002694F.a.01.1.P.Seq	F	M00042591D:H03	CH20COHLV
1725	374235	RTA00002674F.h.13.1.P.Seq	F	M00039141C:E01	CH09LNL
1726	376661	RTA00002689F.e.11.3.P.Seq	F	M00042902D:B08	CH15CON
1727	403014	RTA00002688F.a.07.2.P.Seq	F	M00040368A:A12	CH14EDT
1728	450261	RTA00002691F.e.09.2.P.Seq	F	M00043389D:D07	CH17COHLV
1729	377092	RTA00002678F.o.15.2.P.Seq	F	M00039633D:D05	CH09LNL
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1734	378073	RTA00002681F.j.10.2.P.Seq	F	M00039885C:D01	CH09LNL
1735	379614	RTA00002681F.d.09.1.P.Seq	F	M00039859A:F06	CH09LNL
1736	378994	RTA00002670F.f.03.2.P.Seq	F	M00033376A:C12	CH09LNL
1737	18306	RTA00002708F.a.02.1.P.Seq	F	M00001351A:B02	CH01COH
1738	373347	RTA00002674F.o.07.1.P.Seq	F	M00039180A:A07	CH09LNL
1739	377557	RTA00002671F.i.19.3.P.Seq	F	M00038303D:E07	CH09LNL
1740	402056	RTA00002686F.l.12.1.P.Seq	F	M00040260B:D02	CH13EDT
1741	402424	RTA00002686F.k.15.1.P.Seq	F	M00040253C:A05	CH13EDT
1742	379575	RTA00002679F.p.23.1.P.Seq	F	M00039771C:E11	CH09LNL
1743	22651	RTA00002708F.f.13.1.P.Seq	F	M00004144A:H05	CH01COH
1744	376151	RTA00002675F.n.04.1.P.Seq	F	M00039255C:E12	CH09LNL
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1746	379094	RTA00002672F.o.07.2.P.Seq	F	M00039043B:E01	CH09LNL
1747	38891	RTA00002677F.h.24.2.P.Seq	F	M00039401B:D02	CH09LNL

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1754	380247	RTA00002683F.c.11.2.P.Seq	F	M00040040A:A06	CH09LNL
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1759	376469	RTA00002674F.h.06.1.P.Seq	F	M00039140D:A04	CH09LNL
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1765	379182	RTA00002682F.c.15.1.P.Seq	F	M00039928B:G05	CH09LNL
1766	376200	RTA00002693F.f.08.2.P.Seq	F	M00043203A:B09	CH19COP
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1783	376990	RTA00002683F.f.09.2.P.Seq	F	M00040055D:B01	CH09LNL
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1786	384025	RTA00002670F.k.20.2.P.Seq	F	M00033454A:D09	CH09LNL
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1788	377633	RTA00002684F.g.15.2.P.Seq	F	M00040304B:F06	CH09LNL
1789	430284	RTA00002667F.k.06.1.P.Seq	F	M00032831C:G07	CH08LNH
1790	374773	RTA00002676F.l.22.3.P.Seq	F	M00039316A:C01	CH09LNL
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1794	189139	RTA00002664F.b.14.1.P.Seq	F	M00026851B:F01	CH04MAL
1795	376614	RTA00002677F.c.05.2.P.Seq	F	M00039341D:D07	CH09LNL
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1802	375704	RTA00002676F.h.13.2.P.Seq	F	M00039300C:G04	CH09LNL
1803	399551	RTA00002687F.f.13.1.P.Seq	F	M00040203D:H11	CH14EDT
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4	10924	RTA00002907F.k.12.1.P.Seq	F	M00022224A:C07	CH03MAH
5	45331	RTA00002903F.l.10.1.P.Seq	F	M00007037D:D10	CH02COH
6	42233	RTA00002912F.g.24.1.P.Seq	F	M00027359B:A06	CH04MAL
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13	29706	RTA00002908F.l.22.1.P.Seq	F	M00022487B:A08	CH03MAH
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60	10561	RTA00002899F.h.08.1.P.Seq	F	M00004606D:H09	CH01COH
61	24572	RTA00002893F.l.08.1.P.Seq	F	M00003926A:F11	CH01COH
62	13138	RTA00002888F.m.03.1.P.Seq	F	M00001488C:A03	CH01COH
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90	14665	RTA00002908F.g.07.1.P.Seq	F	M00022425A:C09	CH03MAH
91	10302	RTA00002906F.o.03.1.P.Seq	F	M00022081A:B07	CH03MAH
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155	6635	RTA00002895F.a.07.1.P.Seq	F	M00004057D:G01	CH01COH
156	10220	RTA00002921F.d.09.1.P.Seq	F	M00033360C:A03	CH09LNL
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706	186755	RTA00002912F.i.18.1.P.Seq	F	M00027400D:H02	CH04MAL
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1054	21853	RTA00002896F.g.12.1.P.Seq	F	M00004159C:D10	CH01COH
1055	23439	RTA00002935F.p.01.1.P.Seq	F	M00055402A:H01	CH17COHLV
1056	13060	RTA00002934F.a.19.1.P.Seq	F	M00043529A:B08	CH20COHLV
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1070	16074	RTA00002935F.f.18.1.P.Seq	F	M00054708C:B06	CH17COHLV
1071	13698	RTA00002902F.l.01.1.P.Seq	F	M00006743A:H11	CH02COH
1072	24819	RTA00002922F.j.03.1.P.Seq	F	M00039078B:B03	CH09LNL
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1227	105042	RTA00002917F.o.11.1.P.Seq	F	M00032795C:A03	CH08LNH
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1249	25891	RTA00002909F.p.23.1.P.Seq	F	M00022740C:H11	CH03MAH
1250	4298	RTA00002908F.c.22.1.P.Seq	F	M00022383C:A12	CH03MAH

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1253	12315	RTA00002907F.l.24.2.P.Seq	F	M00022240D:B11	CH03MAH
1254	4930	RTA00002930F.g.04.2.P.Seq	F	M00055810C:D03	CH15CON
1255	12018	RTA00002924F.c.16.1.P.Seq	F	M00039438B:D08	CH09LNL
1256	10501	RTA00002930F.h.23.1.P.Seq	F	M00056024B:F09	CH15CON
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1258	6426	RTA00002927F.b.15.1.P.Seq	F	M00039377B:H09	CH12EDT
1259	2205	RTA00002904F.c.03.1.P.Seq	F	M00007195C:E11	CH02COH
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1261	11928	RTA00002906F.h.05.1.P.Seq	F	M00021971C:B11	CH03MAH
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1268	5565	RTA00002930F.c.02.1.P.Seq	F	M00042908A:F09	CH15CON
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1271	16392	RTA00002899F.a.05.1.P.Seq	F	M00004418B:A11	CH01COH
1272	15797	RTA00002930F.c.23.1.P.Seq	F	M00055456C:H06	CH15CON
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1283	23578	RTA00002930F.a.22.1.P.Seq	F	M00042579A:D09	CH15CON
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1304	113291	RTA00002935F.m.15.1.P.Seq	F	M00055232A:E08	CH17COHLV
1305	13224	RTA00002935F.f.15.1.P.Seq	F	M00054693A:E11	CH17COHLV
1306	14883	RTA00002930F.k.14.1.P.Seq	F	M00056320B:A03	CH15CON
1307	13363	RTA00002935F.a.02.1.P.Seq	F	M00042352D:B03	CH17COHLV
1308	16869	RTA00002889F.c.21.1.P.Seq	F	M00001533C:G11	CH01COH
1309	16	RTA00002935F.a.06.1.P.Seq	F	M00042449B:F05	CH17COHLV
1310	4359	RTA00002903F.j.16.1.P.Seq	F	M00006994C:F06	CH02COH
1311	20726	RTA00002908F.a.17.1.P.Seq	F	M00022363C:D05	CH03MAH
1312	13713	RTA00002924F.l.09.1.P.Seq	F	M00039686C:C01	CH09LNL
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1315	3472	RTA00002922F.n.12.1.P.Seq	F	M00039134D:F08	CH09LNL
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1319	19991	RTA00002908F.h.11.1.P.Seq	F	M00022446C:H06	CH03MAH
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1321	21798	RTA00002932F.b.12.1.P.Seq	F	M00043016B:F09	CH18CON
1322	11303	RTA00002898F.i.11.1.P.Seq	F	M00004359A:E01	CH01COH
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1381	74821	RTA00002890F.p.21.1.P.Seq	F	M00001663A:A12	CH01COH
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1385	23172	RTA00002896F.b.18.1.P.Seq	F	M00004141B:F08	CH01COH
1386	22510	RTA00002886F.l.05.1.P.Seq	F	M00001368A:C02	CH01COH
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1390	1015	RTA00002933F.c.11.1.P.Seq	F	M00043213A:D05	CH19COP
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1392	27830	RTA00002921F.c.07.1.P.Seq	F	M00033344A:B06	CH09LNL
1393	14648	RTA00002898F.j.11.1.P.Seq	F	M00004365C:G11	CH01COH
1394	12585	RTA00002897F.i.20.1.P.Seq	F	M00004269A:F11	CH01COH
1395	15825	RTA00002916F.d.12.1.P.Seq	F	M00032553A:A07	CH08LNH
1396	7043	RTA00002900F.h.07.1.P.Seq	F	M00005014B:F02	CH02COH
1397	29354	RTA00002905F.c.13.1.P.Seq	F	M00007981C:F07	CH03MAH
1398	29703	RTA00002907F.d.24.1.P.Seq	F	M00022144C:E12	CH03MAH
1399	6811	RTA00002913F.b.07.1.P.Seq	F	M00027724D:D04	CH04MAL
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1419	14181	RTA00002908F.n.09.2.P.Seq	F	M00022499D:D08	CH03MAH
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1432	147419	RTA00002906F.g.05.1.P.Seq	F	M00021952B:G06	CH03MAH
1433	12174	RTA00002919F.f.13.1.P.Seq	F	M00033071D:E08	CH08LNH
1434	35608	RTA00002897F.o.24.1.P.Seq	F	M00004296B:D03	CH01COH
1435	2325	RTA00002894F.g.07.1.P.Seq	F	M00003994A:B10	CH01COH
1436	166261	RTA00002908F.l.05.1.P.Seq	F	M00022475D:C07	CH03MAH
1437	5713	RTA00002920F.a.09.1.P.Seq	F	M00033324B:F04	CH08LNH
1438	3624	RTA00002910F.g.06.1.P.Seq	F	M00022901A:C05	CH03MAH
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1440	7768	RTA00002910F.k.22.1.P.Seq	F	M00022992B:G12	CH03MAH
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1443	24376	RTA00002900F.b.07.1.P.Seq	F	M00004836B:C02	CH02COH
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1445	22251	RTA00002926F.c.10.2.P.Seq	F	M00040079B:F06	CH09LNL
1446	12337	RTA00002928F.d.07.1.P.Seq	F	M00040173D:A04	CH13EDT
1447	13623	RTA00002911F.d.08.2.P.Seq	F	M00026842B:A01	CH04MAL
1448	5521	RTA00002887F.j.06.1.P.Seq	F	M00001406B:H09	CH01COH
1449	2193	RTA00002933F.a.13.1.P.Seq	F	M00043077B:F11	CH19COP
1450	773	RTA00002889F.j.02.1.P.Seq	F	M00001551D:H09	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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1453	24011	RTA00002924F.c.17.1.P.Seq	F	M00039440C:G06	CH09LNL
1454	5930	RTA00002911F.f.08.1.P.Seq	F	M00026910B:G06	CH04MAL
1455	21581	RTA00002902F.c.05.1.P.Seq	F	M00005822C:A04	CH02COH
1456	3662	RTA00002925F.c.07.1.P.Seq	F	M00039826D:E04	CH09LNL
1457	4873	RTA00002930F.b.05.1.P.Seq	F	M00042719A:G08	CH15CON
1458	11214	RTA00002896F.h.01.1.P.Seq	F	M00004161A:E08	CH01COH
1459	22888	RTA00002892F.l.09.1.P.Seq	F	M00003837C:D10	CH01COH
1460	15490	RTA00002925F.k.08.1.P.Seq	F	M00039932B:A07	CH09LNL
1461	112819	RTA00002905F.o.13.1.P.Seq	F	M00021676C:G03	CH03MAH
1462	19688	RTA00002896F.l.02.1.P.Seq	F	M00004179D:A12	CH01COH
1463	15132	RTA00002922F.n.20.1.P.Seq	F	M00039138B:G05	CH09LNL
1464	25022	RTA00002914F.i.21.1.P.Seq	F	M00028219B:H05	CH08LNH
1465	16303	RTA00002888F.b.12.1.P.Seq	F	M00001438A:E01	CH01COH
1466	16828	RTA00002897F.b.04.1.P.Seq	F	M00004214A:E05	CH01COH
1467	14295	RTA00002921F.a.18.1.P.Seq	F	M00033296C:C11	CH09LNL
1468	1979	RTA00002930F.f.06.1.P.Seq	F	M00055725D:D09	CH15CON
1469	36248	RTA00002888F.g.05.1.P.Seq	F	M00001460C:E10	CH01COH
1470	5676	RTA00002926F.b.22.2.P.Seq	F	M00040075B:A05	CH09LNL
1471	1239	RTA00002887F.o.21.1.P.Seq	F	M00001428B:C10	CH01COH
1472	7937	RTA00002917F.g.22.1.P.Seq	F	M00032728D:F01	CH08LNH
1473	4483	RTA00002911F.d.22.2.P.Seq	F	M00026856B:G03	CH04MAL
1474	7796	RTA00002925F.c.05.1.P.Seq	F	M00039826B:F09	CH09LNL
1475	17330	RTA00002915F.a.03.1.P.Seq	F	M00028616C:D09	CH08LNH
1476	25620	RTA00002902F.f.09.1.P.Seq	F	M00006631C:A04	CH02COH
1477	20601	RTA00002923F.l.20.1.P.Seq	F	M00039326A:G07	CH09LNL
1478	6205	RTA00002923F.g.21.1.P.Seq	F	M00039258C:C01	CH09LNL
1479	726	RTA00002913F.b.16.1.P.Seq	F	M00027734D:C03	CH04MAL
1480	104999	RTA00002908F.g.17.1.P.Seq	F	M00022435B:G12	CH03MAH
1481	30321	RTA00002919F.o.17.1.P.Seq	F	M00033264B:E06	CH08LNH
1482	5878	RTA00002913F.a.16.1.P.Seq	F	M00027688C:C01	CH04MAL
1483	5944	RTA00002905F.m.07.1.P.Seq	F	M00021649B:A02	CH03MAH
1484	5796	RTA00002908F.i.21.1.P.Seq	F	M00022457A:G05	CH03MAH
1485	3804	RTA00002935F.m.24.1.P.Seq	F	M00055254A:H03	CH17COHLV
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1487	3804	RTA00002935F.n.01.1.P.Seq	F	M00055254A:H03	CH17COHLV
1488	3932	RTA00002915F.o.19.2.P.Seq	F	M00032517C:E10	CH08LNH
1489	16691	RTA00002891F.o.03.1.P.Seq	F	M00003780A:G01	CH01COH
1490	15430	RTA00002900F.g.10.1.P.Seq	F	M00005003D:C02	CH02COH
1491	5637	RTA00002925F.b.18.1.P.Seq	F	M00039820B:F06	CH09LNL
1492	16633	RTA00002897F.g.15.1.P.Seq	F	M00004246B:H07	CH01COH
1493	21826	RTA00002898F.g.06.1.P.Seq	F	M00004344A:G11	CH01COH
1494	22193	RTA00002919F.i.09.1.P.Seq	F	M00033146D:A03	CH08LNH
1495	10720	RTA00002898F.c.14.1.P.Seq	F	M00004320C:E07	CH01COH
1496	22491	RTA00002925F.m.06.1.P.Seq	F	M00040003A:G10	CH09LNL
1497	10423	RTA00002915F.n.13.2.P.Seq	F	M00032507D:G08	CH08LNH
1498	4953	RTA00002916F.h.11.1.P.Seq	F	M00032586C:B04	CH08LNH
1499	185567	RTA00002911F.p.08.1.P.Seq	F	M00027178B:A11	CH04MAL
1500	25605	RTA00002924F.m.22.1.P.Seq	F	M00039710B:A01	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1501	29446	RTA00002906F.m.24.1.P.Seq	F	M00022070B:B04	CH03MAH
1502	9668	RTA00002908F.g.02.1.P.Seq	F	M00022421A:F12	CH03MAH
1503	29446	RTA00002906F.n.01.1.P.Seq	F	M00022070B:B04	CH03MAH
1504	7171	RTA00002887F.m.22.1.P.Seq	F	M00001421B:E07	CH01COH

PP01598 / 200130.512
Table 3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
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22	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
23	<NONE>	<NONE>	<NONE>	548562	GENOME POLYPROTEIN [CONTAINS: RNA REPLICASE ; HELICASE; COAT PROTEIN] 2.7.7.48) - apple stem grooving virus (strain P-209)	9.2
24	<NONE>	<NONE>	<NONE>	416959	EXCISION REPAIR PROTEIN ERCC-6 DNA repair helicase ERCC6 - human >gi\|182181 (L04791) excision repair protein [Homo sapiens]	8.9
25	<NONE>	<NONE>	<NONE>	3327096	(AB014541) KIAA0641 protein [Homo sapiens]	8.7
26	<NONE>	<NONE>	<NONE>	861293	(U28741) F35D2.1 gene product [Caenorhabditis elegans]	7.9
27	<NONE>	<NONE>	<NONE>	3297821	(AL031032) extensin-like protein	5.5
28	<NONE>	<NONE>	<NONE>	2119692	transforming growth factor-beta type III receptor - chicken >gi\|511843 (L01121) transforming growth factor-beta type III receptor [Gallus gallus]	5.1
29	<NONE>	<NONE>	<NONE>	2136028	protein kinase PRK1 - human	5.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
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30	<NONE>	<NONE>	<NONE>	2746912	(AF040659) No definition line found [Caenorhabditis elegans]	4.6
31	<NONE>	<NONE>	<NONE>	2358287	(AF010404) ALR [Homo sapiens]	4.5
32	<NONE>	<NONE>	<NONE>	3877816	(Z96048) predicted using Genefinder; cDNA EST EMBL:D65516 comes from this gene; cDNA EST yk191a5.5 comes from this gene [Caenorhabditis elegans]	4.4
33	<NONE>	<NONE>	<NONE>	4140268	(Y14953) SRCR domain, membrane form 2	4.1
34	<NONE>	<NONE>	<NONE>	1708663	(U51183) transposase [Hydra vulgaris]	4.0
35	<NONE>	<NONE>	<NONE>	1184100	(U45958) pistil extensin-like protein [Nicotiana alata]	3.9
36	<NONE>	<NONE>	<NONE>	121073	GLUCOCORTICOID RECEPTOR (GR)	3.9
37	<NONE>	<NONE>	<NONE>	1718298	(U75698) ORF 45; contains an extended acidic domain; EBV BKRF4 homolog [Kaposi's sarcoma-associated herpesvirus] homolog, conserved in other gamma-herpesviruses	2.6
38	<NONE>	<NONE>	<NONE>	2352538	(AF006564) alcohol dehydrogenase [Drosophila persimilis] persimilis]	1.4
39	<NONE>	<NONE>	<NONE>	3192897	(AF066071) SP85; PsB [Dictyostelium discoideum]	1.4
40	<NONE>	<NONE>	<NONE>	561645	(L33421) This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal	1.0
41	<NONE>	<NONE>	<NONE>	3878857	(Z83120) predicted using Genefinder; cDNA EST EMBL:D35016 comes from this gene; cDNA EST EMBL:D32583 comes from this gene; cDNA EST EMBL:D35258 comes from this gene; cDNA EST EMBL:C11471 comes from this gene; cDNA EST EMBL:C...	1.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
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42	<NONE>	<NONE>	<NONE>	1658571	(U75903) UGT1A7 [Rattus norvegicus]	1.0
43	<NONE>	<NONE>	<NONE>	2338034	(AF005370) putative immediate early protein [Alcelaphine herpesvirus 1]	0.86
44	<NONE>	<NONE>	<NONE>	3043714	(AB011167) KIAA0595 protein [Homo sapiens]	0.42
45	<NONE>	<NONE>	<NONE>	1723710	HYPOTHETICAL 92.7 KD PROTEIN IN ASN2-PHB1 INTERGENIC REGION >gi\|2131678\|pir\|\|S64439 hypothetical protein YGR130c - yeast (Saccharomyces cerevisiae) >gi\|1323215\|gnl\|PID\|e243523 (Z72915) ORF YGR130c [Saccharomyces cerevisiae]	0.40
46	<NONE>	<NONE>	<NONE>	1723710	HYPOTHETICAL 92.7 KD PROTEIN IN ASN2-PHB1 INTERGENIC REGION >gi\|2131678\|pir\|\|S64439 hypothetical protein YGR130c - yeast (Saccharomyces cerevisiae) >gi\|1323215\|gnl\|PID\|e243523 (Z72915) ORF YGR130c [Saccharomyces cerevisiae]	0.38
47	<NONE>	<NONE>	<NONE>	2996117	(AF046125) immediate early 2 [Rat cytomegalovirus]	0.26
48	<NONE>	<NONE>	<NONE>	4151809	(AF102855) synaptic SAPAP-interacting protein Synamon	0.024
49	<NONE>	<NONE>	<NONE>	2773341	(AF040954) putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]	0.017
50	<NONE>	<NONE>	<NONE>	1653522	(D90914) hypothetical protein	3e-04
51	<NONE>	<NONE>	<NONE>	3219965	HYPOTHETICAL 100.6 KD TRP-ASP REPEATS CONTAINING PROTEIN C2C6.04C IN CHROMOSOME I	3e-06
52	<NONE>	<NONE>	<NONE>	4185567	(AF115480) cAMP-dependent Rap1 guanine-nucleotide exchange factor [Mus musculus]	7e-07

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
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53	<NONE>	<NONE>	<NONE>	1176527	PROTEIN C34E10.1 IN CHROMOSOME III >gi\|500724 (U10402) C34E10.1 gene product [Caenorhabditis elegans]	3e-20
54	X85444	G.pallida repetitive DNA element	5.0	2118936	beta-globin - chimpanzee (fragment)	8.6
55	X72961	Synechococcus sp. cpeB, cpeA genes and ORF3	5.0	462569	MICROTUBULE-ASSOCIATED PROTEIN 1A microtubule-associated protein MAP1A - rat >gi\|205538 norvegicus]	2.2
56	U94747	Human WD repeat protein HAN11 mRNA, complete cds	5.0	3875538	(Z67990) similar to cuticle collagen	1.3
57	AF032108	Homo sapiens integrin alpha-7 mRNA, complete cds	5.0	2147194	collagen - Paralvinella grasslei	0.002
58	Z50798	G.gallus mRNA for p52	5.0	3122885	ASPARTYL-TRNA SYNTHETASE synthetase [Bacillus subtilis]	3e-11
59	AB002384	Human mRNA for KIAA0386 gene, complete cds	5.0	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	9e-12
60	X14835	Thermofilum pendens DNA for 16S and 23S ribosomal RNA, tRNA-Met, and tRNA Gly	4.9	<NONE>	<NONE>	<NONE>
61	U87149	Hordeum vulgare nucellin gene, complete cds	4.9	128578	NONSTRUCTURAL PROTEIN NS-S spotted wilt virus (strain CPNH1) non-structural protein [Tomato spotted wilt virus]	2.8
62	D87541	Mus musculus gene for integrin alpha v subunit, promoter region	4.9	136956	HYPOTHETICAL PROTEIN UL61 cytomegalovirus (strain AD169) cytomegalovirus]	0.038
63	U72520	Mus musculus mena protein (Mena) mRNA, complete cds	4.9	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	6e-07

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
64	S79797	enzymatic glycosylation-regulating gene [rats, Sprague-Dawley, streptozotocin diabetic, heart, mRNA, 5010 nt]	4.8	<NONE>	<NONE>	<NONE>
65	AB011102	Homo sapiens mRNA for KIAA0530 protein, partial cds	4.8	138022	RECEPTOR RECOGNIZING PROTEIN gp38 - phage Ox2 >gi\|15126 (X05675) gene 38 (AA 1-266); pid:g15126 [Bacteriophage Ox2]	3.6
66	AF100985	Penaeus monodon phosphopyruvate hydratase mRNA, complete cds	4.8	500615	(D16221) endochitinase [Oryza sativa]	2.8
67	U31756	Bacillus subtilis gamma-aminobutyrate permease cds	4.8	3880699	(AL021471) similar to Eukaryotic aspartyl proteases [Caenorhabditis elegans] Eukaryotic aspartyl proteases [Caenorhabditis elegans]	2.8
68	U25111	Pisum sativum chloroplast processing enzyme mRNA, nuclear gene encoding chloroplast protein, complete cds.	4.8	1800145	(U83658) FH1/FH2 protein homolog [Emericella nidulans]	1.6
69	U00454	Mus musculus Cdx-2 homeobox protein gene, complete cds.	4.7	<NONE>	<NONE>	<NONE>
70	M84166	Hamster c-Ha-ras protein gene, complete cds.	4.7	1710606	RENIN-BINDING PROTEIN (RNBP) protein [Rattus norvegicus]	0.88
71	AF087516	Mus musculus major sperm fibrous sheath protein Pro-mAKAP82 gene, alternative splice exons 1' and 1"	4.6	<NONE>	<NONE>	<NONE>
72	X74160	M.esculenta mRNA for granule-bound starch synthase	4.6	<NONE>	<NONE>	<NONE>
73	M97487	Haloferax volcanii superoxide dismutase (sod2) gene, complete cds.	4.6	2623307	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]	3.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Drosophila				
74	M57889	melanogaster suppressor of sable gene, complete cds.	4.5	<NONE>	<NONE>	<NONE>
75	D49708	Rattus norvegicus mRNA for RNA binding protein	4.5	<NONE>	<NONE>	<NONE>
76	D31853	Yeast GTS1 gene for glycin-threonin/serine repeat protein, complete cds	4.5	2447195	(U42580) NETTF (7x), DETTS (4x) [Paramecium bursaria Chlorella virus 1]	3.3
77	Z47036	Human partial cDNA sequence, clone bs613;	2.9	<NONE>	<NONE>	<NONE>
78	L19660	Rattus norvegicus gastric inhibitory peptide receptor mRNA, complete cds	2.7	2358279	(AF007871) torsinA [Homo sapiens]	2e-07
79	X82841	A.thaliana Aco gene	2.6	483212	immediate-early protein IE110 - human herpesvirus 1 (strain HFEM) (fragment)	8.4
80	X61931	S.purpurascens famA and famB genes for FAS domain and acyl-CoA-dehydrogenases, respectively	2.6	2290534	(U95031) sublingual gland mucin [Homo sapiens]	0.47
81	U13680	Human lactate dehydrogenase-C (LDH-C) mRNA, complete cds.	2.5	2887449	(AB007874) KIAA0414 [Homo sapiens]	3.1
82	AB007869	Homo sapiens KIAA0409 mRNA, partial cds	2.4	3130157	(AB008859) pheromone receptor [Fugu rubripes]	5.4
83	X97479	H.sapiens mas proto-oncogene, 5' region	2.1	<NONE>	<NONE>	<NONE>
84	X98374	R.norvegicus mRNA for KIS protein	1.9	<NONE>	<NONE>	<NONE>
85	AE000710	Aquifex aeolicus section 42 of 109 of the complete genome	1.9	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens mRNA				
86	D30612	for repressor protein, partial cds	1.9	<NONE>	<NONE>	<NONE>
87	Y14321	Homo sapiens PMP69 gene, exons 8,9,10 & 11	1.9	<NONE>	<NONE>	<NONE>
88	D90773	E.coli genomic DNA, Kohara clone #262(30.3-30.5 min.)	1.9	1536816	(D78305) DNA binding protein [Chlorella virus]	7.9
89	AE000991	Archaeoglobus fulgidus section 116 of 172 of the complete genome	1.9	520645	(X79095) pyruvate,orthophosphate dikinase [Flaveria trinervia]	2.7
90	U39476	Rattus norvegicus p95 Vav (Vav) proto-oncogene mRNA, complete cds.	1.9	4158178	(AL023496) hypothetical protein	1.6
91	U28838	Human transcription factor TFIIIB 90 kDa subunit	1.9	2495730	HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 >gi\|1665805\|gnl\|PID\|d1014089 (D87459) Similar to Volbox carteri extensin (S22697) [Homo sapiens]	0.23
92	U20106	Rattus norvegicus synaptotagmin VII mRNA, complete cds.	1.9	478380	UL47h protein - Marek's disease virus	0.23
93	AF071010	Mouse mammary tumor virus putative integrase, env polyprotein, and superantigen mRNA, complete cds	1.9	2781386	(AC004010) similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	4e-33
94	AF061881	Mesocricetus auratus c-fos proto-oncogene protein (c-fos) gene, complete cds	1.8	<NONE>	<NONE>	<NONE>
95	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	1.8	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Horseshoe crab				
96	D14701	mRNA for coagulation factor B, complete cds	1.8	<NONE>	<NONE>	<NONE>
97	M29154	P.falciparum multidrug resistance (MDR) gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
98	L16532	Rattus norvegicus (clone pCNPII) 2',3'-cyclic nucleotide 3'-phosphodiesterase (CNPII) mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
99	AE001434	Plasmodium falciparum chromosome 2, section 71 of 73 of the complete sequence	1.8	<NONE>	<NONE>	<NONE>
100	Z46785	D.melanogaster gene for protamine (mst35Bb).	1.8	<NONE>	<NONE>	<NONE>
101	X69822	P.sylvestris mRNA for glutamine synthetase	1.8	219896	(D90452) l-caldesmon I [Homo sapiens]	9.7
102	U49055	Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds	1.8	2497252	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 (IGFBP-4) (IBP-4) (IGF-BINDING PROTEIN 4) factor-binding protein-4 - sheep (fragment) factor-binding protein-4, IGFBP-4 [sheep, liver, Peptide, 237 aa] [Ovis aries]	2.5
103	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	1.8	4204267	(AC005223) 55585 [Arabidopsis thaliana]	2.4
104	U66987	Pandorina morum internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	1.8	2635909	(Z99121) permease [Bacillus subtilis]	1.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human polymorphic				
105	X58033	MspI site DNA (D3S3 locus)	1.8	2136878	keratin KAP5.5 - sheep (fragment) >gi\|313722	0.65
106	U15780	Human p82 (ST5) mRNA, alternatively spliced, complete cds	1.8	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	0.64
107	AF038535	Homo sapiens synaptotagmin VII mRNA, partial cds	1.8	457927	(U00690) calcium channel alpha-1 subunit [Drosophila melanogaster]	0.51
108	AF052134	Homo sapiens clone 23585 mRNA sequence	1.8	232263	HOMEOBOX PROTEIN HOX-D1 (HOX-4.9)	0.28
109	X75208	H.sapiens HEK2 mRNA for protein tyrosine kinase receptor.	1.8	1730198	GROWTH-ARREST-SPECIFIC PROTEIN 1 gene product [Homo sapiens]	0.22
110	AB013896	Xenopus laevis mRNA for SOX-D, complete cds	1.8	2494501	TRANSCRIPTION FACTOR FKH-4 factor [Mus musculus]	0.17
111	D16947	Human HepG2 3' region cDNA, clone hmd6b10	1.8	3413870	(AB007923) KIAA0454 protein [Homo sapiens]	0.002
112	D13547	Mouse DNA, T early alpha (TEA) region	1.8	3393018	(AL031174) hypothetical protein	5e-08
113	M35498	Woodchuck c-myc protein gene, exon 1.	1.8	3183405	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi\|2370504\|gnl\|PID\|e339194 pombe] >gi\|3451305\|gnl\|PID\|e1316730 (AL031324) very hypothetical protein [Schizosaccharomyces pombe]	8e-10
114	M84166	Hamster c-Ha-ras protein gene, complete cds.	1.8	3386622	(AC004665) unknown protein [Arabidopsis thaliana]	2e-10
115	U33135	Mychodea carnosa 18S ribosomal RNA gene, complete sequence	1.8	3334982	(AC005306) R27216_1 [Homo sapiens]	3e-22
116	U84003	Homo sapiens putative tumor suppressor (BIN1) gene, exons 7-12	1.7	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
117	AE001121	Borrelia burgdorferi (section 7 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
118	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
119	U82064	Angiostrongylus cantonensis adult-specific muscle protein-1 gene, partial cds	1.7	<NONE>	<NONE>	<NONE>
120	AF041836	Buchnera aphidicola plasmid pLeu-Sg, complete plasmid sequence	1.7	<NONE>	<NONE>	<NONE>
121	M87479	Lymnaea stagnalis FMRFamide gene, mature peptides.	1.7	<NONE>	<NONE>	<NONE>
122	M55163	Xenopus laevis fibroblast growth factor receptor mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
123	S57565	histamine H2-receptor [rats, Genomic, 1928 nt]	1.7	<NONE>	<NONE>	<NONE>
124	M27256	Simian immunodeficiency virus (SIV) pol region.	1.7	<NONE>	<NONE>	<NONE>
125	U31516	Human chromosome 8 anonymous clone pBS8-165	1.7	<NONE>	<NONE>	<NONE>
126	X12671	Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1	1.7	<NONE>	<NONE>	<NONE>
127	AF009054	Paeonia suffruticosa ssp. spontanea alcohol dehydrogenase 1B (Adh1B) gene, partial cds	1.7	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
128	AF046917	Mus musculus transketolase gene, exon 6 and partial cds	1.7	<NONE>	<NONE>	<NONE>
129	D89053	Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds	1.7	<NONE>	<NONE>	<NONE>
130	U57968	Staphylothermus marinus surface layer-associated STABLE protease gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
131	L39072	Bovine herpesvirus 1 (clone p95) UL24 homologue gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
132	X04980	Drosophila simulans retrotransposon 297 5'-LTR and flanks (pWK1020)	1.7	<NONE>	<NONE>	<NONE>
133	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
134	X04434	Human mRNA for insulin-like growth factor I receptor	1.7	<NONE>	<NONE>	<NONE>
135	U07890	Mus musculus C57BL/6J epidermal surface antigen (mesa) mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
136	D26163	Human tyrosinase gene, 5'-flanking region cell-specific transcription)	1.7	<NONE>	<NONE>	<NONE>
137	AF093818	Panorpa nipponensis NADH dehydrogenase subunit 5 gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.7	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis				
138	D50560	mRNA for cytochrome P-450, complete cds	1.7	<NONE>	<NONE>	<NONE>
139	AF083488	Mus musculus phospholipase D1 (PLD1) gene, exons 18 and 19, complete sequence	1.7	<NONE>	<NONE>	<NONE>
140	AF100694	Mus musculus Pontin52 mRNA, complete cds	1.7	<NONE>	<NONE>	<NONE>
141	M73749	Streptococcus salivarius thermophilus beta-D-galactose (lacZ) gene, complete cds. > :: gb\|M63636\|STRLACZZ Streptococcus thermophilus beta-D-galactosidase (lacZ) gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
142	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	2183023	(U84971) unknown [Homo sapiens]	9.2
143	L01983	Human type IV sodium channel alpha polypeptide	1.7	130504	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR ... virus (strain D)	9.2
144	L19731	Plecotus rafinesquii mitochondrial cytochrome b gene, 5' end.	1.7	3327096	(AB014541) KIAA0641 protein [Homo sapiens]	9.1
145	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	2183023	(U84971) unknown [Homo sapiens]	8.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
146	L27218	Bos taurus serum amine oxidase mRNA, complete cds. > oxidase=amiloride-binding protein homolog [cattle, liver, mRNA, 2664 nt]	1.7	1174459	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 6 (IL-4 STAT) >gi\|559855 (U16031) IL-4 Stat [Homo sapiens]	7.1
147	Z49868	Caenorhabditis elegans cosmid W07E11, complete sequence [Caenorhabditis elegans]	1.7	4204263	(AC005223) 40409 [Arabidopsis thaliana]	6.7
148	AL022271	Caenorhabditis elegans cosmid F32F2, complete sequence [Caenorhabditis elegans]	1.7	2497969	PERIPLASMIC NITRATE REDUCTASE PRECURSOR >gi\|1086107\|pir\|\|S50163 nitrate reductase large chain precursor, periplasmic - Thiosphaera pantotropha >gi\|600093 (Z36773) periplasmic nitrate reductase large subunit [Paracoccus denitrificans]	6.7
149	U43844	Mus musculus cyclin D3 gene, complete cds	1.7	3861490	(AF062037) capsid protein precursor [Thosea asigna virus]	5.1
150	Z25464	S.cerevisiae UNF1, LTV1, MRP8, CYB3 and TGL1 genes, complete CDS's	1.7	1255404	(U53151) weak similarity to cytochrome b [Caenorhabditis elegans]	4.1
151	U77846	Human elastin gene, partial cds and partial 3'UTR	1.7	3355682	(AL031124) putative secreted lyase	4.0
152	X62880	S.scrofa mRNA for calcium release channel (CRC)	1.7	3327080	(AB014533) KIAA0633 protein [Homo sapiens]	4.0
153	Y00067	Human gene for neurofilament subunit M (NF-M)	1.7	479829	heterogeneous ribonuclear particel protein homolog - Caenorhabditis elegans similarity to RNA recognition motifs [Caenorhabditis elegans]	3.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
154	X68393	D.melanogaster gene for Beta-tubulin, exons 1 and 2	1.7	2342682	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb\|X95577). [Arabidopsis thaliana]	3.8
155	AB012284	Shuttle vector pAUR123 gene for Aur1-C, complete cds	1.7	417704	POL POLYPROTEIN (ORF1A/1B) [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; HELICASE; PROTEASE]	3.8
156	M96633	Rattus norvegicus mitochondrial intermediate peptidase (MIP) mRNA, complete cds.	1.7	2314209	(AE000613) H. pylori predicted coding region HP1054	3.1
157	U49055	Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds	1.7	2497252	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 (IGFBP-4) (IBP-4) (IGF-BINDING PROTEIN 4) factor-binding protein-4 - sheep (fragment) factor-binding protein-4, IGFBP-4 [sheep, liver, Peptide, 237 aa] [Ovis aries]	3.0
158	Y15907	Mus musculus mRNA for myc-intron-binding protein-1	1.7	912776	iduronate-2-sulfatase, IDS {EC 3.1.6.13} Peptide Mutant, 550 aa]	3.0
159	U67600	Methanococcus jannaschii section 142 of 150 of the complete genome	1.7	2982355	(AF052252) fork head domain protein FKD9 [Danio rerio]	3.0
160	AF013759	Homo sapiens calumein (Calu) mRNA, complete cds	1.7	2982355	(AF052252) fork head domain protein FKD9 [Danio rerio]	2.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AL021066) Similarity to Human mRNA product	
161	AF062915	Arabidopsis thaliana putative transcription factor (MYB90) mRNA, complete cds	1.7	3878065	KIAA0077 (TR:Q14997); cDNA EST yk243h8.5 comes from this gene; cDNA EST yk243h8.3 comes from this gene; cDNA EST yk359h4.5 comes from this gene [Caenorhabditis elegans] >gi\|3880318\|gnl\|PID\|e1349839 (Z81133) Similarity to Human mRNA product KIAA0077 (TR:Q14997); cDNA EST yk243h8.5 comes from this gene; cDNA EST yk243h8.3 comes from this gene; cDNA EST yk359h4.5 comes from this gene	2.3
162	X87526	H.sapiens genomic DNA (chromosome 3; clone NL3003R)	1.7	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	2.3
163	AC005573	Homo sapiens chromosome 5, PAC clone 202e13	1.7	2465540	(AF005632) phosphodiesterase I/nucleotide pyrophosphatase beta [Homo sapiens]	1.8
164	D83402	Homo sapiens gene for prostacyclin synthase, exon 10 and complete cds	1.7	627608	steroid hormone receptor TR3 - human sapiens]	1.7
165	AF053700	Homo sapiens deltex (Dx) mRNA, complete cds	1.7	2662089	(AB007864) KIAA0404 [Homo sapiens]	1.7
166	AF043225	Mus musculus 6-pyruvoyl-tetrahydropterin synthase (Pts) mRNA, complete cds	1.7	2352538	(AF006564) alcohol dehydrogenase [Drosophila persimilis] persimilis]	1.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
167	U52917	Thermus aquaticus thermophilus NADH dehydrogenase I subunits NQO7 NQO6, NQO5, NQO4, NQO2, NQO1, NQO3, NQO8, NQO9, NQO10, NQO11, NQO12, NQO13, and NQO14, complete cds.	1.7	2564334	(AB006631) The human homolog of mouse Cux-2 [Homo sapiens]	1.0
168	X72222	M.musculus gene for serotonin 2 receptor	1.7	3875796	(Z73425) Similarity to Yeast hypothetical YIK9 protein (SW:YIK9_YEAST); cDNA EST EMBL:T01252 comes from this gene; cDNA EST EMBL:D33205 comes from this gene; cDNA EST EMBL:D33955 comes from this gene; cDNA EST EMBL:D35484 co...	1.0
169	U23186	Crotalus scutulatus PLA2-like pseudogene	1.7	853971	(X83413) DR5 [Human herpesvirus 6] >gi\|853972 (X83413) DR5 [Human herpesvirus 6]	0.99
170	M83118	Mus musculus factor VIII-associated protein (f8a) mRNA, complete cds.	1.7	3201617	(AC004669) hypothetical protein [Arabidopsis thaliana]	0.80
171	M38347	E.coli ATP-dependent proteinase (lon) gene, complete cds.	1.7	4140322	(AL031282) dJ283E3.3.2 (Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase)) (isoform beta 2-2) [Homo sapiens]	0.78
172	U28838	Human transcription factor TFIIIB 90 kDa subunit	1.7	2495730	HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 >gi\|1665805\|gnl\|PID\|d1014089 (D87459) Similar to Volbox carteri extensin (S22697) [Homo sapiens]	0.62

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
173	U72487	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds	1.7	544411	GLYCOPROTEIN GP100 PRECURSOR (P29F8) discoideum]	0.35
174	AE000718	Aquifex aeolicus section 50 of 109 of the complete genome	1.7	2497569	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3) (HEPARIN-BINDING GROWTH FACTOR RECEPTOR) >gi\|2117851\|pir\|\|I55363 fibroblast growth factor receptor 3 - mouse >gi\|199145 (M81342) fibroblast growth factor receptor 3 [Mus musculus]	0.34
175	AF016897	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (OsGDI2) mRNA, complete cds	1.7	125362	MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR (CSF-1-R) (FMS PROTO-ONCOGENE) (C-FMS) factor 1 receptor - cat >gi\|163855 (J03149) M-CSF receptor [Felis domesticus]	0.34
176	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.7	85058	muscarinic acetylcholine receptor - fruit fly acetylcholine receptor [Drosophila melanogaster]	0.20
177	AF077352	Chlamydomonas reinhardtii myosin heavy chain	1.7	728901	ACROSOMAL PROTEIN SP-10 PRECURSOR SP-10 - western baboon >gi\|298488\|bbs\|127113 (S56458) SP-10=intraacrosomal protein [Papio papio=baboons, Peptide, 285 aa] [Papio hamadryas]	0.20
178	Z92788	Caenorhabditis elegans cosmid F53B8, complete sequence [Caenorhabditis elegans]	1.7	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi\|3258651 elegans]	0.068

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(X87883) mitochondrial capsule	
179	AF002217	Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene, complete cds	1.7	1143538	selenoprotein [Rattus norvegicus] >gi\|1354135 (U48702) mitochondia associated cysteine-rich protein SMCP	0.039
180	D30749	Rat mRNA for protein tyrosine phosphatase	1.7	1228035	(D83776) The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region. [Homo sapiens]	0.008
181	M15202	Rat fast skeletal TnT gene encoding troponin T isoforms, complete cds.	1.7	731172	SKIN SECRETORY PROTEIN XP2 PRECURSOR	4e-04
182	L07592	Human peroxisome proliferator activated receptor mRNA, complete cds.	1.7	4033414	PUTATIVE IMPORTIN BETA-4 SUBUNIT	2e-06
183	U64031	Dendrobium crumenatum ACC synthase gene, complete cds	1.7	3122885	ASPARTYL-TRNA SYNTHETASE synthetase [Bacillus subtilis]	2e-11
184	AF034970	Homo sapiens docking protein (DOK-2) mRNA, complete cds	1.7	2289097	(U78737) alpha(1,3)fucosyltransferase [Cricetulus griseus]	8e-12
185	Z12839	L.longiflorum mRNA encoding calmodulin. > :: gb\|L18912\|LILCALMODU Lilium longiflorum calmodulin mRNA, complete cds.	1.7	2511747	(AF023270) probable transcriptional regulator dre4	4e-12

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
186	X53459	Equine arteritis virus (EAV) RNA genome > :: emb\|A45589\|A45589 Sequence 1 from Patent WO9519438 > :: emb\|A58849\|A58849 Sequence 1 from Patent WO9700963 > :: gb\|AR013959\|AR013959 Sequence 1 from patent US 5773235	1.7	3979817	~~(Z70683) Weak similarity to~~ Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 comes from this gene; cDNA EST EMBL:C12822 comes from this gene; cDNA EST yk408c2.3 comes from this gene; cDNA EST yk408c2.5 ... Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 comes from this gene; cDNA EST EMBL:C12822 comes from this gene; cDNA EST yk408c2.3 comes from this gene; cDNA EST yk408c2.5 ...	1e-14
187	K02668	E. coli ddl gene encoding D-alanine:D-alanine ligase and ftsQ and ftsA genes, complete cds, and ftsZ gene, 5' end.	1.7	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES...	2e-19
188	AB008375	Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds	1.7	2496945	HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II >gi\|733603 (U23484) No definition line found [Caenorhabditis elegans]	1e-19
189	L36603	Pseudomonas cepacia (clone Psudom70-1) heat shock protein 70 (hsp70) gene, complete cds	1.7	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	6e-20

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 75.5 KD	
190	Z49760	P.blakesleeanus mRNA GTP cyclohydrolase I	1.7	1731181	PROTEIN C14A4.3 IN CHROMOSOME II >gi\|3874230\|gnl\|PID\|e1351618 protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans]	3e-21
191	U52428	Human fatty acid synthase gene, partial cds	1.7	4226073	(AF125443) contains similarity to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	6e-25
192	U12767	Human mitogen induced nuclear orphan receptor	1.6	<NONE>	<NONE>	<NONE>
193	Z63478	H.sapiens CpG DNA, clone 85a12, forward read cpg85a12.ft1a .	1.6	<NONE>	<NONE>	<NONE>
194	AF084375	Homo sapiens inversin protein, exons 8 and 9	1.6	<NONE>	<NONE>	<NONE>
195	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.6	<NONE>	<NONE>	<NONE>
196	AF084375	Homo sapiens inversin protein, exons 8 and 9	1.6	<NONE>	<NONE>	<NONE>
197	U24217	Kluyveromyces lactis RNA polymerase II largest subunit gene, partial cds	1.6	<NONE>	<NONE>	<NONE>
198	AE000580	Helicobacter pylori 26695 section 58 of 134 of the complete genome	1.6	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
199	X62083	H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue > :: gb\|M80613\|HUMFSHG Human homolog of Drosophila female sterile homeotic mRNA, complete cds.	1.6	<NONE>	<NONE>	<NONE>
200	M28064	Plasmodium brasilianum DNA homologous to the histidine-rich knob protein region of Plasmodium falciparum.	1.6	457495	(M26647) ORF X [Saccharomyces cerevisiae]	8.4
201	U03114	Streptomyces albus lipase precursor (lip) gene, complete cds, and unidentified 5' ORF and 3' ORF, partial cds.	1.6	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	7.8
202	U88422	Strix varia oocyte maturation factor Mos (c-mos) proto-oncogene, partial cds	1.6	137618	VITAMIN D3 RECEPTOR (VDR) receptor [Rattus norvegicus]	6.4
203	M68519	Human pulmonary surfactant-associated protein SP-A (SFTP1) gene, complete cds.	1.6	3875423	(Z38112) E03A3.6 [Caenorhabditis elegans]	4.9
204	AF044575	Homo sapiens transcription factor POU4F3	1.6	2133625	GABA transport protein - tobacco hornworm	4.7
205	L48476	Homo sapiens (subclone 3_e10 from P1 H21) DNA sequence.	1.6	3687297	(AJ005588) 5-epi-aristolochene synthase	4.6
206	M18630	Rat CNS 2',3'-cyclic nucleotide 3-phosphodiesterase	1.6	3880315	(Z81133) Similarity to Human mRNA product KIAA0077 (TR:Q14997) [Caenorhabditis elegans]	3.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
207	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1.6	267068	TUMOR-ASSOCIATED ANTIGEN L6	3.6
208	U53448	Babesia microti heat shock protein 70 (hsp70) gene, complete cds	1.6	1255429	(U53155) strong similarity to the carboxyl two-thirds of valyl-tRNA synthetases [Caenorhabditis elegans]	2.2
209	AF084367	Homo sapiens inversin protein mRNA, complete cds	1.6	1730076	PROBABLE SERINE/THREONINE-PROTEIN KINASE CY49.28 >gi\|1370255\|gnl\|PID\|e247094 (Z73966) pknJ	1.2
210	D55635	Yeast dis1+ gene for p93dis1, complete cds	1.6	3128353	(AF010496) maltose transport inner membrane protein	1.2
211	AF035756	Streptomyces sp. 2-dehydro-3-deoxyphosphohepton ate aldolase gene, partial cds	1.6	853971	(X83413) DR5 [Human herpesvirus 6] >gi\|853972 (X83413) DR5 [Human herpesvirus 6]	0.97
212	X73479	O.cuniculus rPTPA mRNA	1.6	3413810	(Y17034) Bassoon [Mus musculus]	0.94
213	X98330	H.sapiens mRNA for ryanodine receptor 2	1.6	2072986	(U95142) putative G-protein-coupled receptor G-protein-coupled receptor [Arabidopsis thaliana]	0.73
214	X64194	P.anserina FMR1 gene exons 1 and 2	1.6	128014	NECDIN >gi\|91129\|pir\|\|JN0148 necdin, brain - mouse >gi\|200020 (M80840) necdin [Mus musculus]	0.42
215	Z92788	Caenorhabditis elegans cosmid F53B8, complete sequence [Caenorhabditis elegans]	1.6	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi\|3258651 elegans]	0.19
216	AE000888	Methanobacterium thermoautotrophicum from bases 1098908 to 1112186 (section 94 of 148) of the complete genome	1.6	462415	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC) >gi\|346520\|pir\|\|S27387 interferon alpha receptor type 1 - bovine >gi\|432	0.001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
217	AB008375	Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds	1.6	2496945	HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II >gi\|733603 (U23484) No definition line found [Caenorhabditis elegans]	1e-18
218	M25312	Orang-utan involucrin gene, complete cds.	1.6	3875131	(Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	3e-26
219	AB012882	Cyprinus carpio mRNA for MyoD, complete cds	1.5	<NONE>	<NONE>	<NONE>
220	U29487	Caenorhabditis elegans cosmid C09C7	1.5	<NONE>	<NONE>	<NONE>
221	X74760	M.musculus mRNA for Notch 3	1.5	1364094	integral membrane protein - Streptomyces pristinaespiralis >gi\|872306 (X84072) integral membrane protein [Streptomyces pristinaespiralis]	4.3
222	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	1.5	121855	EXOGLUCANASE II PRECURSOR cellulose 1,4-beta cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [Trichoderma reesei]	4.3
223	U42391	Human myosin-IXb mRNA, complete cds	1.5	3688428	(AJ011534) sucrose synthase	4.2
224	M92296	Pongo pygmaeus gamma-1 and gamma-2 globin genes, complete cds.	1.5	186413	(M13144) inhibin A [Homo sapiens]	0.22
225	X94144	C.japonica mRNA for QNR-71 protein	1.5	2745737	(AF029791) UDP-Gal:betaGlcNAc beta 1,3-galactosyltranferase-II [Mus musculus]	3e-08

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
226	AB014557	Homo sapiens mRNA for KIAA0657 protein, partial cds	1.5	1212992	(X90568) Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE [Homo sapiens]	4e-13
227	AF000948	Borrelia burgdorferi oligopeptide permease homolog OppAIV (oppAIV) gene, complete cds	1.3	<NONE>	<NONE>	<NONE>
228	AF057287	Mus musculus RAB/Rip protein mRNA, partial cds	1.3	2498005	MYC PROTO-ONCOGENE PROTEIN (C-MYC) proto-oncogene [Sus scrofa]	2.6
229	U38951	Drosophila melanogaster vacuolar ATPase subunit E	1.1	<NONE>	<NONE>	<NONE>
230	AF027148	Homo sapiens myogenic determining factor 3	1.1	3172134	(U90209) RNA polymerase II largest subunit [Bonnemaisonia hamifera]	2.3
231	AF079310	Mus musculus histone deacetylase 3 (Hdac3) gene, exons 4 through 15 and complete cds	1.0	1657601	(U66220) unknown [Nannocystis exedens]	0.25
232	X52134	P.radiata lac gene for laccase	0.95	996020	(X91638) BRM protein [Gallus gallus]	0.31
233	D89016	Human mRNA for Neuroblastoma, complete cds	0.93	<NONE>	<NONE>	<NONE>
234	X76392	C.familiaris VIP36 (vesicular integral-membrane protein of 36 kDa) mRNA	0.93	4176446	(AL022238) dJ1042K10.2.1 (novel protein with probable rabGAP domains and Src homology domain 3)	7e-81
235	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.90	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					EGT2 PROTEIN PRECURSOR	
236	AE000991	Archaeoglobus fulgidus section 116 of 172 of the complete genome	0.90	1176579	(EARLY GT TRANSCRIPT 2) >gi\|1362345\|pir\|\|S55862 probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae) cerevisiae] >gi\|1302445\|gnl\|PID\|e239572 (Z71603) ORF YNL327w [Saccharomyces cerevisiae]	6.9
237	Z35922	S.cerevisiae chromosome II reading frame ORF YBR053c	0.86	<NONE>	<NONE>	<NONE>
238	U47331	Rattus norvegicus metabotropic glutamate receptor 4b mRNA, complete cds.	0.82	1550703	(Z80225) hypothetical protein Rv2662	4.1
239	X72810	H.sapiens Ig germline kappa-chain gene variable region (L3)	0.69	3023063	(AF052587) F14 [Xylella fastidiosa]	6.7
240	Z11700	Escherichia coli genes faeG, faeH, faeI, faeJ and IS629-like insertion sequence. > :: emb\|Z11710\|ECFAE HIJ E.coli faeH, faeI and faeJ genes encoding FaeH, FaeI and FaeJ proteins	0.69	2347188	(AC002338) laccase isolog [Arabidopsis thaliana] thaliana]	3.9
241	U71597	Phrynosoma douglassii NADH dehydrogenase subunit 4 (ND4) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.65	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					GLUTAMYL-TRNA	
242	Z77798	Ammonia species LSU rRNA gene (partial; isolate Tr S 5; clone 16)	0.64	1174506	SYNTHETASE glutamate--tRNA ligase (EC 6.1.1.17) - Haemophilus influenzae (strain Rd KW20) >gi\|1573240 (U32713) glutamyl-tRNA synthetase (gltX) [Haemophilus influenzae Rd]	1.2
243	D25542	Human mRNA for golgi antigen gcp372, complete cds	0.64	111230	ultra-high-sulfur keratin 1 - mouse	1e-05
244	M80234	Cow dopamine transporter mRNA, putative cds.	0.64	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	8e-06
245	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.64	2833239	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi\|530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	2e-14
246	X51754	Human U266 rearranged DNA for lambda-immunoglobulin light chain	0.63	2072301	(U95102) mitotic phosphoprotein 90 [Xenopus laevis]	1.5
247	AE001554	Helicobacter pylori, strain J99 section 115 of 132 of the complete genome	0.62	<NONE>	<NONE>	<NONE>
248	Z64067	H.sapiens CpG DNA, clone 96e7, reverse read cpg96e7.rt1a .	0.62	<NONE>	<NONE>	<NONE>
249	AJ223768	Pinus sylvestris microsatellite DNA, clone SPAC11.5	0.62	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
250	AJ011592	Bacteriophage P1 ban gene	0.62	2493689	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN deltoides] >gi\|2143326\|gnl\|PID\|e319090 (Y13328) 10kDa phosphoprotein [Populus deltoides]	7.9
251	AF027151	Xenopus laevis survival of motor neuron protein interacting protein 1 (SIP1) mRNA, complete cds	0.62	4007790	(AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]	2.0
252	AJ000376	Helobdella triserialis mRNA for actin	0.62	1117968	(U40763) CARS-Cyp [Homo sapiens] sapiens]	0.90
253	M69231	Rat thymosin beta 4 gene (pTB4G),intron.	0.62	4176370	(AC005058) similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	6e-51
254	AB021638	Homo sapiens X11L2 mRNA for X11-like protein 2, complete cds	0.61	<NONE>	<NONE>	<NONE>
255	D26470	Bacteroides gingivalis DNA for arginyl endopeptidase, complete cds	0.61	<NONE>	<NONE>	<NONE>
256	J04737	A.thaliana ATPase gene, complete cds.	0.61	<NONE>	<NONE>	<NONE>
257	U06756	Bos taurus clone bm1308 microsatellite and are-1p repeat region.	0.61	1922280	(Y09905) snail like protein [Gallus gallus]	0.51
258	S75756	p15=cyclin D-dependent kinases 4 and 6-binding protein/p15 product {exon/intron 1} [human, brain tumors, Genomic, 753 nt]	0.61	484938	hypothetical protein 253 - Streptomyces griseus plasmid pSG1 (fragment)	0.13
259	L39837	Drosophila melanogaster tumor supressor (warts) mRNA exons 1-8, complete cds.	0.61	3875131	(Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	1e-09

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AF125443) contains similarity	
260	U52428	Human fatty acid synthase gene, partial cds	0.61	4226073	to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	2e-26
261	X15292	Plasmodium falciparum gene for heat-shock protein pPf203	0.60	<NONE>	<NONE>	<NONE>
262	AB020663	Homo sapiens mRNA for KIAA0856 protein, partial cds	0.60	470341	(U00043) No definition line found [Caenorhabditis elegans]	5.7
263	U68723	Human checkpoint suppressor 1 mRNA, complete cds	0.60	544375	GALACTOSE-BINDING PROTEIN REGULATOR glucose/galactose binding protein regulator - Agrobacterium tumefaciens >gi\|142228 (L10424) glucose/galactose binding protein regulator	5.7
264	M32687	S.griseus sporulation protein genes 1590 and 1422.	0.60	2582017	(AF012871) Merg1a' [Mus musculus]	3.3
265	AJ005331	Homo sapiens NKCC2 gene, exon 4, isoform B	0.60	3128353	(AF010496) maltose transport inner membrane protein	1.5
266	U14103	Mus musculus RGL protein mRNA, complete cds.	0.60	4099845	(U90533) serine protease inhibitor [Streptomyces fradiae]	0.098
267	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.59	3282851	(AF047897) ankyrin-like protein HGE-ANK [Ehrlichia sp. BDS]	5.5
268	AE000872	Methanobacterium thermoautotrophicum from bases 896604 to 912784 (section 78 of 148) of the complete genome	0.59	401553	HYPOTHETICAL 24.5 KD PROTEIN IN NADB-SRMB INTERGENIC REGION	4.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					hypothetical protein - human herpesvirus 4 reading frame 1 [Human herpesvirus 4] 2 [Human herpesvirus 4] >gi\|1334838\|gnl\|PID\|e25079 4 [Human herpesvirus 4] >gi\|1334840\|gnl\|PID\|e25081 6 [Human herpesvirus 4] >gi\|1334842\|gnl\|PID\|e25067 8 [Human herpesvirus 4] >gi\|1334844\|gnl\|PID\|e25069 10 [Human herpesvirus 4] >gi\|1334846\|gnl\|PID\|e25071 12 [Human herpesvirus 4]	
269	L11871	Gallus gallus achaete-scute homologue (ASH) mRNA, complete cds.	0.59	628110		4.2
270	AF017114	Oryctolagus cuniculus glycogen synthase mRNA, complete cds	0.59	728856	NITROGENASE IRON-IRON PROTEIN ALPHA CHAIN (NITROGENASE COMPONENT I) (DINITROGENASE) capsulatus >gi\|312238 (X70033) alternative nitrogenase	2.4
271	AF027807	Homo sapiens beta-casein (CSN2) gene, complete cds	0.59	3252932	(AF067155) truncated rev protein [Human immunodeficiency virus type 1]	1.5
272	U81787	Human Wnt10B mRNA, complete cds	0.59	3875538	(Z67990) similar to cuticle collagen	1.4
273	U76036	Apteryx australis 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.59	4193356	(AF055088) ATP-binding cassette; PsaB [Streptococcus pneumoniae]	0.83
274	AB014564	Homo sapiens mRNA for KIAA0664 protein, partial cds	0.59	1709851	PTB-ASSOCIATED SPLICING FACTOR (PSF) long form - human >gi\|38458 (X70944) PTB-associated splicing factor [Homo sapiens]	0.17
275	AF044171	Homo sapiens cyclin-dependent kinase inhibitor 2D (CDKN2D) gene, partial cds	0.59	3925213	(AL032626) Y37D8A.17 [Caenorhabditis elegans]	3e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
276	L19640	Saccharomyces cerevisiae cdc2/cdc28-related protein kinase gene, complete cds.	0.59	3880115	(Z81130) T23G11.9 [Caenorhabditis elegans]	1e-21
277	Z80999	Human DNA sequence from cosmid E140G5 on chromosome 22, complete sequence [Homo sapiens]	0.58	<NONE>	<NONE>	<NONE>
278	Y11108	H.sapiens WNT8B gene	0.58	<NONE>	<NONE>	<NONE>
279	U80001	Sphyraena idiastes lactate dehydrogenase A	0.58	<NONE>	<NONE>	<NONE>
280	Z49637	S.cerevisiae chromosome X reading frame ORF YJR137c	0.58	<NONE>	<NONE>	<NONE>
281	X64467	H.sapiens ALAD gene for porphobilinogen synthase	0.58	<NONE>	<NONE>	<NONE>
282	X74506	G.gallus hox B3 mRNA	0.58	<NONE>	<NONE>	<NONE>
283	U68040	Cochliobolus heterostrophus polyketide synthase	0.58	<NONE>	<NONE>	<NONE>
284	AF089084	Arabidopsis thaliana putative auxin efflux carrier protein (PIN1) mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
285	U38481	Rattus norvegicus ROK-alpha mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
286	AF017656	Homo sapiens G protein beta 5 subunit mRNA, complete cds	0.58	3236249	(AC004684) hypothetical protein [Arabidopsis thaliana]	9.2
287	M96234	Human glutathione transferase class mu number 4	0.58	1280073	(U55366) Similar to cuticle collagen [Caenorhabditis elegans]	7.1
288	AB002339	Human mRNA for KIAA0341 gene, partial cds	0.58	861293	(U28741) F35D2.1 gene product [Caenorhabditis elegans]	7.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
289	U11295	Neisseria gonorrhoeae carbamoyl phosphate synthetase (glutamine) small subunit (carA) and large subunit (carB) genes, complete cds.	0.58	2425135	(AF020283) DG2044 gene product [Dictyostelium discoideum]	5.3
290	D80001	Human mRNA for KIAA0179 gene, partial cds	0.58	4097223	(U49836) gamma-glutamyl transpeptidase precursor [Brugia malayi]	4.1
291	Z11700	Escherichia coli genes faeG, faeH, faeI, faeJ and IS629-like insertion sequence. > :: emb\|Z11710\|ECFAE HIJ E.coli faeH, faeI and faeJ genes encoding FaeH, FaeI and FaeJ proteins	0.58	2347188	(AC002338) laccase isolog [Arabidopsis thaliana] thaliana]	3.2
292	M77350	Mouse hair keratin A1 (MHKA1) gene, complete cds.	0.58	141165	HYPOTHETICAL 8.3 KD PROTEIN >gi\|62179	3.2
293	X63787	T.thermophila gene for snRNA U3-2	0.58	2826900	(AB004461) DNA polymerase alpha catalytic subunit [Oryza sativa]	3.1
294	D63881	Human mRNA for KIAA0160 gene, partial cds	0.58	1934730	(U95036) germin-like protein [Arabidopsis thaliana]	3.1
295	U39378	Gymnocarena mexicana 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial RNA, partial sequence	0.58	2194131	(AC002062) Similar to Synechocystis antiviral protein	3.1
296	X87987	P.pastoris PRC1 gene > :: dbj\|E12103\|E12103 DNA encoding precursor of protease from Pichia pastoris	0.58	3914197	OCCLUDIN >gi\|1276983 (U49221) occludin [Canis familiaris] >gi\|1589181\|prf\|\|2210347D occludin [Canis familiaris]	3.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
297	X75782	A.thaliana (L.Heynh.) chloroplast mRNA for recombinant APS-kinase	0.58	1732444	(D38529) DRPLA protein [Homo sapiens]	2.4
298	M64848	Mouse platelet-derived growth factor B chain musculus platelet-derived growth factor beta-chain (sis) gene, exon 5.	0.58	3025832	(AF055985) pyrrolidone-rich antigen [Onchocerca volvulus]	1.4
299	AE001460	Helicobacter pylori, strain J99 section 21 of 132 of the complete genome	0.58	2827198	(AF037454) ubiquitin protein ligase [Mus musculus]	1.1
300	X65720	M.musculus gene for protein kinase C-gamma (exon1 and exon 2)	0.58	418395	CHD1 PROTEIN >gi\|320737\|pir\|\|S30818 hypothetical protein YER164w - yeast (Saccharomyces cerevisiae) >gi\|603404 (U18917) Chd1p: transcriptional regulator [Saccharomyces cerevisiae]	1.1
301	AF043130	Arabidopsis thaliana lactate dehydrogenase	0.58	3024637	SEX-DETERMINING REGION Y PROTEIN determining protein [Mus	0.62
302	D28116	Human genes for collagen type IV alpha 5 and 6, exon 1 and exon 1'	0.58	1458250	(U64835) T09D3.3 [Caenorhabditis elegans]	0.36
303	AE001075	Archaeoglobus fulgidus section 32 of 172 of the complete genome	0.58	2276333	(Z97991) hypothetical protein Rv0336	0.36
304	AF003948	Rhodococcus opacus chloromuconate cycloisomerase transposase homolog genes, complete cds	0.58	477072	mucin 7 precursor, salivary - human	0.28
305	U10692	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds.	0.58	3287858	HOMEOBOX PROTEIN HOX-C11	0.054

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
306	AF003948	Rhodococcus opacus chloromuconate cycloisomerase transposase homolog genes, complete cds	0.58	3551821	(AF058803) mucin 4 [Homo sapiens]	0.041
307	X99350	H.sapiens HFH4 gene, exon 1 and joined CDS	0.58	137483	VAV PROTO-ONCOGENE >gi\|55221 (X64361) proto-oncogene [Mus musculus]	0.024
308	AJ234282	Homo sapiens mRNA for Ig heavy chain variable region, clone C	0.58	3264846	(AC003682) R27945_2 [Homo sapiens]	0.018
309	AF079310	Mus musculus histone deacetylase 3 (Hdac3) gene, exons 4 through 15 and complete cds	0.58	1657601	(U66220) unknown [Nannocystis exedens]	0.014
310	AF019367	Human thiopurine methyltransferase (TPMT) gene, exons 6 and 7	0.58	3283352	(AF063020) lens epithelium-derived growth factor [Homo sapiens]	0.011
311	X65720	M.musculus gene for protein kinase C-gamma (exon1 and exon 2)	0.58	1790878	(U38291) microtubule-associated protein 1a [Homo sapiens]	0.008
312	AB011155	Homo sapiens mRNA for KIAA0583 protein, partial cds	0.58	1351166	SYNAPSINS IA AND IB >gi\|163713	0.006
313	X63692	H.sapiens mRNA for DNA	0.58	1817548	(D84307) phosphoethanolamine cytidylyltransferase [Homo sapiens]	0.001
314	U53746	Feline immunodeficiency virus isolate FIV-Pco336-8 pol polyprotein (pol) gene, partial cds	0.58	2246532	(U93872) ORF 73, contains large complex repeat CR 73	2e-05
315	K00436	Rattus norvegicus (clone rt1-1) pseudo-Gly-tRNA gene.	0.58	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	1e-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
316	S79632	HSF2=heat shock factor 2 {alternatively spliced, splice junction region} [mice, CBA/J, testis, Genomic, 120 nt, segment 2 of 3]	0.58	4038594	(AJ222798) tDET1 protein [Lycopersicon esculentum]	3e-06
317	D43964	Rat liver mRNA for Kan-1, complete cds	0.58	1280135	(U55376) coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	1e-08
318	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.58	2833239	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi\|530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	3e-13
319	AB001466	Homo sapiens mRNA for Efs1, complete cds	0.58	2943716	(D45027) 25 kDa trypsin inhibitor [Homo sapiens]	2e-14
320	Z11701	Saccharomyces cerevisiae IRE1 gene for putative protein kinase.	0.58	3880115	(Z81130) T23G11.9 [Caenorhabditis elegans]	9e-21
321	Z49535	S.cerevisiae chromosome X reading frame ORF YJR035w	0.58	4106562	(Z83819) dJ146H21.2 (similar to CYTOCHROME B-245 HEAVY CHAIN) [Homo sapiens]	3e-33
322	M62506	S.cerevisiae DBF20 gene, complete cds.	0.57	<NONE>	<NONE>	<NONE>
323	X05944	Yeast PSS gene for phosphatidylserine synthetase	0.57	<NONE>	<NONE>	<NONE>
324	D38536	Snail gene for ADP-ribosyl cyclase, complete cds	0.57	<NONE>	<NONE>	<NONE>
325	Z75004	S.cerevisiae chromosome XV reading frame ORF YOR096w	0.57	<NONE>	<NONE>	<NONE>
326	L77034	Homo sapiens (subclone 10_e10 from P1 H16) DNA sequence.	0.57	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
327	D37887	Cyprinus carpio c-myc gene for c-Myc, complete cds	0.57	<NONE>	<NONE>	<NONE>
328	AB014562	Homo sapiens mRNA for KIAA0662 protein, partial cds	0.57	197406	(M57576) Ig kappa chain [Mus musculus]	8.9
329	Z69651	Human DNA sequence from cosmid L75B9, Huntington's Disease Region, chromosome 4p16.3	0.57	1079280	chaperonin containing TCP-1 complex gamma chain - African clawed frog >gi\|793886 (X84990) Cctg	8.9
330	D89285	Mesocricetus auratus mRNA for inter-alpha trypsin inhibitor heavy chain 1, complete cds	0.57	134132	RYANODINE RECEPTOR, SKELETAL MUSCLE	6.9
331	Z48951	S.cerevisiae chromosome XVI cosmid 9723	0.57	4210432	(AJ130783) APC2 protein [Mus musculus]	5.3
332	X95573	A.thaliana mRNA for salt-tolerance zinc finger protein	0.57	1174828	TYROSINE DECARBOXYLASE 2 4.1.1.25) - parsley >gi\|169671 (M96070) tyrosine decarboxylase [Petroselinum	5.2
333	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.57	465646	PROBABLE ABC TRANSPORTER ATP-BINDING PROTEIN IN NTRA/RPON 5'REGION (ORF1) Azorhizobium caulinodans >gi\|311388 (X69959) ORF1	4.0
334	AE001116	Borrelia burgdorferi (section 2 of 70) of the complete genome	0.57	2314735	(AE000653) Na+/H+ antiporter (nhaA) [Helicobacter pylori 26695]	4.0
335	Z34291	R.norvegicus mRNA for putative chloride channel.	0.57	1350832	DNA-DIRECTED RNA POLYMERASE I SECOND LARGEST SUBUNIT (RNA POLYMERASE I SUBUNIT 2) chain RPA2 - Euplotes octocarinatus (SGC9) >gi\|578407 octocarinatus]	3.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z81063) similar to Actinin-type	
336	D88255	Homo sapiens A30 Vk germline gene, partial cds	0.57	3875983	actin-binding domain containing proteins [Caenorhabditis elegans]	3.0
337	AF037261	Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds	0.57	1397341	(U61955) Similar to kinesin-like protein; coded for by C. elegans cDNA yk184h5.3; coded for by C. elegans cDNA yk184h5.5; coded for by C. elegans cDNA yk13d7.3; coded for by C. elegans cDNA yk13d7.5; coded for by C. elegans cDNA yk31e1.5; co... >gi\|3493541 (AF057567) kinesin-like protein ZEN-4a [Caenorhabditis elegans]	2.3
338	U26595	Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds	0.57	2773160	(AF039656) neuronal tissue-enriched acidic protein [Homo sapiens]	2.3
339	X69903	R.norvegicus mRNA for interleukin 4 receptor	0.57	2649193	(AE001009) quinone-reactive Ni/Fe-hydrogenase B-type cytochrome subunit (hydC) [Archaeoglobus fulgidus]	1.8
340	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w	0.57	1458319	(U64846) F47D2.5 gene product [Caenorhabditis elegans]	1.4
341	AJ131469	Foot-and-mouth disease virus O vp1 gene, strain O/A/58	0.57	91206	proline-rich protein - mouse (fragment) musculus]	1.4
342	AF011360	Mus musculus regulator of G-protein signaling 7 (RGS7) mRNA, complete cds	0.57	542514	gelsolin - American lobster	0.80
343	AF011360	Mus musculus regulator of G-protein signaling 7 (RGS7) mRNA, complete cds	0.57	1078946	gelsolin - American lobster >gi\|452313 gelsolin [Homarus americanus]	0.80

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
344	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	0.57	559526	(X77466) 98.8kD polyprotein [Strawberry latent ringspot virus]	0.79
345	U81523	Human endometrial bleeding associated factor mRNA, complete cds	0.57	211499	(K01702) HMW/LMW collagen subunit precursor [Gallus gallus]	0.79
346	U46561	Tetrahymena thermophila polyubiquitin (TTU3) gene, complete cds, and RNA polymerase II subunit 2 (RPB2) gene, partial cds	0.57	2506493	HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION >gi\|882654 (U29579) alternate gene name ygcB; ORF_f888 [Escherichia coli] >gi\|1789119	0.60
347	X95543	C.japonica mRNA for legumin (clone CjLeg31)	0.57	1709261	NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M) >gi\|1083164\|pir\|\|S55395 neurofilament protein M - rabbit (fragment) >gi\|854353	0.46
348	Y17282	Homo sapiens mRNA for cytokeratin type II	0.57	3044086	(AF055904) unknown [Myxococcus xanthus]	0.45
349	X00716	Frog mRNA fragment for alpha-A2-crystallin	0.57	3406654	(AF079369) transcriptional repressor TUP1 [Dictyostelium discoideum]	0.20
350	X53238	Klebsiella sp. bacteriophage K11 gene 1 for RNA polymerase	0.57	1228093	(Z46913) polyketide synthase	0.16
351	X99012	H.sapiens FUS gene, exon 12	0.57	243898	(S78897) GOR=antigenic epitope [chimpanzees, Peptide, 427 aa] [Pan]	0.090
352	AL008711	Human DNA sequence from PAC 390N22 on chromosome Xp22.2	0.57	1469545	(U53585) fibronectin attachment protein [Mycobacterium avium]	0.053
353	S74506	SOX9 [human, fetal brain, Genomic, 1494 nt, segment 3 of 3]	0.57	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nulcear division RFT1 protein (SP:P38206)	0.017

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
354	D25542	Human mRNA for golgi antigen gcp372, complete cds	0.57	4063399	(AF102575) cell surface protein DTFA [Dictyostelium discoideum]	0.005
355	AB015426	Mus musculus mRNA for alpha1,3-fucosyltransferase IX, complete cds	0.57	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	7e-11
356	X51394	Xenopus mRNA for APEG protein, containing a highly repetitive amino acid sequence	0.57	1929056	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]	9e-12
357	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.57	2833239	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi\|530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	3e-13
358	AB001466	Homo sapiens mRNA for Efs1, complete cds	0.57	2943716	(D45027) 25 kDa trypsin inhibitor [Homo sapiens]	2e-14
359	Y00760	Rabbit mRNA for adult fast skeletal troponin-C	0.57	2576348	(AC002400) Glutamyl tRNA synthetase [Homo sapiens]	2e-28
360	X95153	H.sapiens brca2 gene exon 3 > :: emb\|A62778\|A62778 Sequence 19 from Patent WO9719110	0.57	3419847	(AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]	2e-55
361	X85967	B.vulgaris mRNA for betavulgin	0.56	<NONE>	<NONE>	<NONE>
362	U09251	Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA synthetase (serS) genes, partial cds.	0.56	<NONE>	<NONE>	<NONE>
363	V00158	Chloroplast Euglena gracilis genes coding for transfer RNAs specific for threonine, glycine, methionine, serine and glutamine.	0.56	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Clostridium				
364	D88151	perfringens DNA for D-alanine:D-alanine ligase, cortical fragment-lytic enzyme	0.56	<NONE>	<NONE>	<NONE>
365	U67478	Methanococcus jannaschii section 20 of 150 of the complete genome	0.56	<NONE>	<NONE>	<NONE>
366	L23800	Tachyglossus aculeatus beta-globin homolog (HBB) gene, complete cds	0.56	<NONE>	<NONE>	<NONE>
367	AB011129	Homo sapiens mRNA for KIAA0557 protein, partial cds	0.56	<NONE>	<NONE>	<NONE>
368	L77034	Homo sapiens (subclone 10_e10 from P1 H16) DNA sequence.	0.56	<NONE>	<NONE>	<NONE>
369	Z47202	C.albicans gene for TFIIIB (BRF1) subunit.	0.56	<NONE>	<NONE>	<NONE>
370	U53868	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds	0.56	<NONE>	<NONE>	<NONE>
371	AF041259	Homo sapiens breast cancer putative transcription factor (ZABC1) mRNA, complete cds	0.56	<NONE>	<NONE>	<NONE>
372	L42636	Plasmodium falciparum variant-specific surface protein (var-7) mRNA, complete cds.	0.56	2213557	(Z97052) hypothetical protein	8.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
373	U96180	Human protein tyrosine phosphatase (TEP1) mRNA, complete cds	0.56	731016	THIOREDOXIN REDUCTASE thioredoxin reductase (NADPH) [Coxiella burnetii]	8.7
374	L76259	Homo sapiens PTS gene, complete cds	0.56	2369863	(Y12225) Spi-1/PU.1 transcription factor	6.7
375	AF045946	Mus musculus D16Jhu17 YAC 98B3 acentric end, partial sequence	0.56	2130017	hypothetical protein - common sunflower protein [Helianthus annuus]	5.1
376	X97986	M.musculus mRNA for desmocollin type 1	0.56	4038031	(AC005936) hypothetical protein [Arabidopsis thaliana]	3.9
377	X79437	M.musculus whey acidic protein (WAP) gene, exon 1	0.56	549670	SPINDLE POLE BODY COMPONENT SPC42 yeast (Saccharomyces cerevisiae) >gi\|486054 (Z28042) ORF YKL042w [Saccharomyces cerevisiae] >gi\|666098 (X71621) hypothetical 42.3 kD protein [Saccharomyces cerevisiae]	3.9
378	M27902	Rat cardiac specific sodium channel alpha-subunit mRNA, complete cds.	0.56	585234	ENDOGLUCANASE G PRECURSOR 3.2.1.-) CelCCG precursor - Clostridium cellulolyticum cellulolyticum]	3.9
379	AF036696	Caenorhabditis elegans cosmid F15B10	0.56	546071	gp70=envelope protein {endogenous provirus} host=cat lymphoid tissues, Peptide, 445 aa]	3.6
380	Z99102	Caenorhabditis elegans cosmid B0331, complete sequence [Caenorhabditis elegans]	0.56	603664	(U14101) putative reverse transcriptase; ORF2; encodes aa motifs conserved in reverse transcriptases; most closely related reverse transcriptases are those of non-LTR retrotransposons. The 3' 901 bp of this CDS are identical to the 3' 901 bp ...	3.0
381	L27850	Equus caballus (clone T131) T-cell receptor DNA, V-region.	0.56	1079150	transcription factor shn - fruit fly	1.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 113.1 KD	
382	X97986	M.musculus mRNA for desmocollin type 1	0.56	2497227	PROTEIN IN PRE5-FET4 INTERGENIC REGION >gi\|1072409 (Z54141) unknown	1.7
383	AF087455	Didelphis virginiana G protein receptor kinase 2 mRNA, complete cds	0.56	1213453	(U12964) contains ankyrin-like repeats; similar to human desmoplakin repeat region [Caenorhabditis elegans]	1.3
384	D80011	Human mRNA for KIAA0189 gene, complete cds	0.56	226535	protease [Hepatitis B virus]	1.1
385	AJ002272	Mus musculus mRNA for HAP1-A protein, 3' region	0.56	3327158	(AB014572) KIAA0672 protein [Homo sapiens]	1.0
386	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	0.56	628431	coat protein - strawberry latent ringspot virus	0.77
387	X02770	Mouse Thy-1.2 gene 5' untranslated region and exon 1	0.56	3327046	(AB014516) KIAA0616 protein [Homo sapiens]	0.59
388	AF038575	Schizosaccharomyces pombe Wiskott-Aldrich Syndrome protein homolog (wsp1+) gene, complete cds, and BTF3/beta-NAC gene, partial sequence	0.56	88466	salivary proline-rich phosphoprotein precursor PRH1 (allele PIF) - human >gi\|190484 (K03203) prepro salivary proline-rich protein [Homo sapiens] >gi\|190512	0.35
389	X56747	Rat mRNA for fetal intestinal lactase-phlorizin hydrolase precursor, partial	0.56	2072742	(Z48674) chitinase homologue [Sesbania rostrata]	0.23
390	Y12072	G.arboreum mRNA for farnesyl pyrophosphate synthase	0.56	296670	(X07882) Po protein [Homo sapiens]	0.20
391	S75756	p15=cyclin D-dependent kinases 4 and 6-binding protein/p15 product {exon/intron 1} [human, brain tumors, Genomic, 753 nt]	0.56	1082743	protein kinase (EC 2.7.1.37) SPRK - human sapiens] >gi\|1090771\|prf\|2019437A protein Tyr kinase I	0.15

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Equus caballus type				
392	U62528	II collagen mRNA, complete cds	0.56	461671	[Segment 1 of 2] COLLAGEN ALPHA 1(I) CHAIN	0.030
393	X96877	C.reinhardtii mRNA for unknown lumenal polypeptide	0.56	3341678	(AC003672) putative zinc finger protein [Arabidopsis thaliana]	5e-09
394	S78788	cGATA-3 [chickens, liver, Genomic, 979 nt, segment 4 of 4]	0.56	2661590	(AL009196) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=59.41; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA950019; 2-match_description=LD29959.5prime LD Drosophila melanogas...	2e-11
395	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.56	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	6e-12
396	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.56	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	4e-13
397	AE000716	Aquifex aeolicus section 48 of 109 of the complete genome	0.56	3688350	(AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8) [Homo sapiens]	3e-66
398	Z36079	S.cerevisiae chromosome II reading frame ORF YBR210w	0.55	<NONE>	<NONE>	<NONE>
399	Y17267	Mus musculus mRNA for ubiquitin conjugating enzyme	0.55	<NONE>	<NONE>	<NONE>
400	AC001461	Homo sapiens (subclone 2_g5 from BAC H107) DNA sequence	0.55	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Alouatta seniculus				
401	AF019079	breast and ovarian susceptibility (BRCA1) gene, partial cds	0.55	<NONE>	<NONE>	<NONE>
402	M90058	Human serglycin gene, exons 1,2, and 3.	0.55	<NONE>	<NONE>	<NONE>
403	AB013469	Mus musculus CLM2 gene for cytohesin 2, complete and partial cds, alternative splicing	0.55	1729760	(Z68152) chitinase [Gossypium hirsutum]	8.6
404	AJ011592	Bacteriophage P1 ban gene	0.55	2493689	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN deltoides] >gi\|2143326\|gnl\|PID\|e319090 (Y13328) 10kDa phosphoprotein [Populus deltoides]	6.6
405	Z15118	T.brucei kinetoplast maxicircle variable region DNA	0.55	2970432	(AF049132) NADH dehydrogenase subunit 5 [Florometra serratissima]	6.5
406	Z48951	S.cerevisiae chromosome XVI cosmid 9723	0.55	4210432	(AJ130783) APC2 protein [Mus musculus]	4.9
407	U78726	Homo sapiens mad protein homolog Smad2 gene, promoter, exon 1a and exon 1b	0.55	3319290	(AF055994) thyroid hormone receptor-associated protein complex component TRAP220 [Homo sapiens]	4.9
408	AG001389	Homo sapiens genomic DNA, 21q region, clone: 9H11Bm42	0.55	125684	KRUEPPEL PROTEIN >gi\|72899\|pir\|\|TWFF Krueppel gap protein - fruit fly (Drosophila sp.) melanogaster] >gi\|224875\|prf\|\|1202348A Krueppel gene	3.8
409	M27640	Plasmodium vivax major blood stage surface antigen gene, partial cds.	0.55	549453	X-LINKED PEST-CONTAINING TRANSPORTER transporter - human >gi\|458255 (U05321) X-linked PEST-containing transporter [Homo sapiens]	3.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Fugu rubripes mRNA for sodium channel alpha subunit, partial cds				
410	D37977		0.55	1435038	(D38024) ORF [Homo sapiens]	3.7
411	M88505	Ostertagia ostertagi cathepsin B-like cysteine protease gene, partial cds.	0.55	3941277	(AF000900) p45 [Rattus norvegicus]	2.9
412	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.55	2570154	(AB008376) 17-kDa PKC-potentiated inhibitory protein of PP1 [Sus scrofa]	2.8
413	U89241	Human mibp gene, partial cds	0.55	4097465	(U62253) 16kDa secretory protein [Sus scrofa]	2.2
414	AF027151	Xenopus laevis survival of motor neuron protein interacting protein 1 (SIP1) mRNA, complete cds	0.55	4007790	(AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]	1.7
415	AF006821	Bufo marinus natriuretic peptide receptor C mRNA, partial cds	0.55	2245075	(Z97343) GTP-binding RAB2A protein	1.7
416	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, llabiiM, llabiiR genes and orfX	0.55	3386334	(AF035120) type I procollagen pro-alpha 2 chain [Canis familiaris]	1.3
417	U38307	Mus musculus collagen alpha-1 type 1 gene, 5' flanking region, partial sequence.	0.55	1362802	gastric mucin - human (fragment) >gi\|547517	1.3
418	D13473	Mouse mRNA for Rad51 protein	0.55	1374698	(D83032) nuclear protein, NP220 [Homo sapiens]	1.3
419	AF045238	Bungarus fasciatus acetylcholinesterase gene, alternatively spliced products, partial cds	0.55	3261734	(Z94752) hypothetical protein Rv1004c	0.99
420	AE000795	Methanobacterium thermoautotrophicum from bases 1 to 10208 (section 1 of 148) of the complete genome	0.55	186396	(M94131) mucin [Homo sapiens]	0.97

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Y.lipolytica SEC62			(Z81068) F25H5.2	
421	X99537	gene	0.55	3876397	[Caenorhabditis elegans]	0.58
422	U08147	Aquilegia sp. phytochrome (PHYB/D) gene, partial cds.	0.55	2338024	(AF005370) ribonucleotide-reductase, large subunit	0.57
423	Z56586	H.sapiens CpG DNA, clone 12c8, reverse read cpg12c8.rt1d .	0.55	3320122	(U46007) espin [Rattus norvegicus]	0.44
424	U39442	Mus musculus glutamine:fructose-6-phosphate amidotransferase (GFAT) gene, 5' region and partial cds	0.55	282600	hypothetical protein - Mycoplasma hyorhinis	0.43
425	K02298	Rat chymotrypsin B (chyB) gene, complete cds.	0.55	3413810	(Y17034) Bassoon [Mus musculus]	0.33
426	X84792	M.musculus clusterin gene	0.55	1652475	(D90905) hypothetical protein	0.25
427	U00185	Capra aegagrus Saanen and Weisse Edel breeds DR beta-chain antigen binding domain, MHC class II DRB	0.55	2507136	SUBTILIN BIOSYNTHESIS PROTEIN SPAB	0.19
428	Z54946	H.sapiens CpG DNA, clone 178a12, reverse read cpg178a12.rt1a .	0.55	807646	(M17294) unknown protein [Human herpesvirus 4]	0.065
429	AF031650	Oryctolagus cuniculus anion exchanger 3 brain isoform (AE3) mRNA, complete cds	0.55	1778210	(U68412) fibrillar collagen [Arenicola marina]	0.044
430	M25579	Bovine adenylyl cyclase Type I mRNA, complete cds.	0.55	2649040	(AE000997) conserved hypothetical protein [Archaeoglobus fulgidus]	0.023
431	Z48796	H.sapiens Ski-W mRNA for helicase	0.55	330452	(M14708) DNA polymerase [Human cytomegalovirus]	0.023

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
432	M80234	Cow dopamine transporter mRNA, putative cds.	0.55	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	4e-04
433	U91616	Human I kappa B epsilon (IkBe) mRNA, complete cds	0.55	3875577	(Z68314) similar to G-protein; cDNA EST EMBL:C11959 comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene [Caenorhabditis elegans] >gi\|388036-4\|gnl\|PID\|e1349948 (Z83016) similar to G-protein; cDNA EST EMBL:C11959 comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene [Caenorhabditis elegans]	7e-06
434	D10910	Arabidopsis thaliana Atpk7 gene for serine/threonine protein kinase, complete cds	0.55	3876072	(Z81505) Similarity to Metanococcus hypothetical protein 0682 (TR:Q58095) [Caenorhabditis elegans]	4e-42
435	L22013	Swinepox virus complete ORFS C20L-C1L > :: gb\|I58297\|I58297 Sequence 14 from patent US 5651972	0.54	<NONE>	<NONE>	<NONE>
436	Z92653	Human immunodeficiency virus type 1 env gene	0.54	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
437	K01992	E.coli phosphate-repressible periplasmic phosphate-binding protein (phoS), peripheral membrane proteins (pstC, pstB and phoU) and integral membrane protein (pstA) genes, complete cds.	0.54	<NONE>	<NONE>	<NONE>
438	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	0.54	<NONE>	<NONE>	<NONE>
439	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.54	<NONE>	<NONE>	<NONE>
440	X12591	E.coli plasmid DNA for colicin E9	0.54	<NONE>	<NONE>	<NONE>
441	U73679	Caenorhabditis elegans YNK1-a mRNA, complete cds	0.54	<NONE>	<NONE>	<NONE>
442	Z93990	Unidentified bacterium DNA for 16S ribosomal RNA	0.54	<NONE>	<NONE>	<NONE>
443	X85967	B.vulgaris mRNA for betavulgin	0.54	757836	(Z37980) ORF12 [Escherichia coli]	8.3
444	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.54	151377	(M80653) tetraheme [Pseudomonas stutzeri]	6.2
445	X71800	H.sapiens gene for 5S rRNA (640 bp) > :: emb\|X71801\|HS5SR640B H.sapiens gene for 5S rRNA (640 bp)	0.54	3322653	(AE001216) T. pallidum predicted coding region TP0369	2.7
446	U89241	Human mibp gene, partial cds	0.54	4097465	(U62253) 16kDa secretory protein [Sus scrofa]	2.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
447	L16013	Rattus norvegicus Q-like gene sequence	0.54	3087760	(AJ005583) p75 protein [Crypthecodinium cohnii]	0.95
448	U60275	Capra hircus skeletal muscle voltage-gated chloride channel gClC-1 mRNA, partial cds	0.54	1781344	(Y10438) FK506 polyketide synthase	0.95
449	U36795	Myxococcus xanthus rfbABC O-antigen biosynthesis operon, rfbA, rfbB, and rfbC genes, complete cds.	0.54	3877232	(Z81540) predicted using Genefinder	0.74
450	AF053091	Drosophila melanogaster eyelid (eld) mRNA, complete cds	0.54	2144110	zinc finger protein RIZ - rat >gi\|949996	0.14
451	V00602	Genome of the bacteriophage fd (Inoviridae).	0.54	2661620	(AL009197) hypothetical protein	0.11
452	U60800	Human semaphorin (CD100) mRNA, complete cds	0.54	125682	KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN) >gi\|109116\|pir\|\|A36686 ultra-high-sulfur keratin - sheep >gi\|1306 (X55294) ultra high-sulphur keratin protein [Ovis aries]	0.003
453	X85969	S.coelicolor secD, secF & apt genes	0.54	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	7e-06
454	Y08265	H.sapiens mRNA for DAN26 protein, partial	0.54	3875131	(Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	5e-12

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Hydromantes				
455	U89613	platycephalus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.53	<NONE>	<NONE>	<NONE>
456	AF034597	Habrobracon hebetor cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products	0.53	<NONE>	<NONE>	<NONE>
457	K02653	Yeast (S.cerevisiae) tau repetitive element and Cys-tRNA.	0.53	<NONE>	<NONE>	<NONE>
458	X53416	Human mRNA for actin-binding protein (filamin)	0.53	2134839	bullous pemphigoid antigen 2 - human	6.2
459	M55545	Drosophila subobscura alchohol dehydrogenase (Adh) gene, and alchohol dehydrogenase (Adh-dup) gene, complete cds's.	0.53	2136865	hair keratin cysteine rich protein - sheep	2.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
460	U19362	Methanobacterium thermoautotrophicum methylene-tetrahydromethanopterin dehydrogenase (mtd), imidazoleglycerol-phosphate dehydrogenase (hisB), and putative ferredoxin (fdxA) genes, complete cds, orf9 gene, partial cds, orfs ...	0.53	731969	HYPOTHETICAL 91.6 KD PROTEIN IN HXT8-CRT1 INTERGENIC REGION >gi\|1078261\|pir\|\|S50773 probable membrane protein YJL212c - yeast (Saccharomyces cerevisiae) >gi\|496950 (Z34098) ORF [Saccharomyces cerevisiae] >gi\|1015596 (Z49487) ORF YJL212c	0.54
461	AB011527	Rattus norvegicus mRNA for MEGF1, complete cds	0.53	417037	GERM CELL-LESS PROTEIN fruit fly (Drosophila melanogaster) >gi\|157490 (M97933) germ cell-less protein [Drosophila melanogaster]	3e-06
462	U64313	Bacillus firmus MsyB gene, 5' upstream region and partial cds	0.52	<NONE>	<NONE>	<NONE>
463	AF008590	Caenorhabditis elegans paraquat responsive protein (CePqM132) mRNA, complete cds	0.52	<NONE>	<NONE>	<NONE>
464	L10245	Mus saxicola spermidine/spermine N1-acetyltransferase (SSAT) gene, complete cds.	0.52	<NONE>	<NONE>	<NONE>
465	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.52	124263	INSULIN-LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) >gi\|69361\|pir\|\|IGHU1B insulin-like growth factor IB precursor - human prepropeptide [Homo sapiens]	7.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
466	AL021066	elegans cosmid H31B20, complete sequence [Caenorhabditis elegans]	0.52	2589162	(D88451) aldehyde oxidase [Zea mays]	6.0
467	AF038588	Porphyra linearis 18S ribosomal RNA gene, 3' partial sequence	0.52	1055055	(U39850) coded for by C. elegans cDNA yk37g1.5; coded for by C. elegans cDNA yk5c9.5; coded for by C. elegans cDNA yk1a9.5; alternatively spliced form of F52C9.8b	4.6
468	AE001125	Borrelia burgdorferi (section 11 of 70) of the complete genome	0.52	4115827	(AB021287) polyprotein [Hepatitis G virus]	2.0
469	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.52	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	0.002
470	U90177	Aplysia californica ubiquitin carboxyl-terminal hydrolase (Ap-uch) mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
471	Z28304	S.cerevisiae chromosome XI reading frame ORF YKR079c	0.51	<NONE>	<NONE>	<NONE>
472	Z92837	Caenorhabditis elegans cosmid R03E1, complete sequence [Caenorhabditis elegans]	0.51	123506	HYDROPHOBIC SEED PROTEIN (HPS)	7.6
473	D13803	Mouse mRNA for RecA-like protein MmRad51, complete cds	0.51	3327228	(AB014607) KIAA0707 protein [Homo sapiens]	4.5
474	X07187	Pea hsp21 mRNA	0.51	3328678	(AE001299) hypothetical protein [Chlamydia trachomatis]	4.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		CCAAT/enhancer-				
475	S63168	binding protein delta=transcription factor CRP3 homolog [human, prostate carcinoma cell line LNCaP, Genomic, 1594 nt]	0.51	1653215	(D90911) apolipoprotein N-acyltransferase [Synechocystis sp.]	1.2
476	U67078	Xenopus laevis C2-HC type zinc finger protein X-MyT1 mRNA, complete cds	0.51	3850320	(AF067520) PITSLRE protein kinase beta SV2 isoform [Homo sapiens]	0.17
477	L38933	Homo sapiens GT198 mRNA, complete ORF	0.51	3219965	HYPOTHETICAL 100.6 KD TRP-ASP REPEATS CONTAINING PROTEIN C2C6.04C IN CHROMOSOME I	0.059
478	AF001000	Lycopersicon esculentum polygalacturonase 1	0.50	<NONE>	<NONE>	<NONE>
479	Z28304	S.cerevisiae chromosome XI reading frame ORF YKR079c	0.50	<NONE>	<NONE>	<NONE>
480	X97225	Oncorhynchus keta IGF-II gene	0.50	<NONE>	<NONE>	<NONE>
481	AJ001388	Homo Sapiens, RP58 cDNA for complete mRNA	0.50	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo Sapiens, RP58				
481	AJ001388	cDNA for complete mRNA	0.50	<NONE>	<NONE>	<NONE>
482	M86626	P.occultum 23S ribosomal RNA, partial cds.	0.50	<NONE>	<NONE>	<NONE>
483	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.50	1722856	CHROMOSOME ASSEMBLY PROTEIN XCAP-E African clawed frog >gi\|563814 (U13674) XCAP-E [Xenopus laevis]	3.2
484	AF031663	Mus musculus striatin mRNA, complete cds	0.50	179521	(M63730) BPAG2 [Homo sapiens]	3.2
485	U32729	Haemophilus influenzae Rd section 44 of 163 of the complete genome	0.50	3875699	(Z92829) F10A3.15 [Caenorhabditis elegans]	0.65
486	AF067198	Dictyostelium discoideum clone 9.10 Tdd-3 and RED repetitive elements, partial sequence	0.50	2494740	HYPOTHETICAL 28.3 KD PROTEIN IN GBD 5'REGION (ORF4) >gi\|2120954\|pir\|\|I39562 ORF4 - Alcaligenes eutrophus >gi\|695274 (L36817) ORF4	0.008
487	M23442	Human interleukin 4 (IL-4) gene, complete cds.	0.49	<NONE>	<NONE>	<NONE>
488	U16367	Caenorhabditis elegans POU homeobox protein CEH-18 (ceh-18) mRNA, complete cds.	0.47	3786409	(AF098499) contains similarity to Saccharomyces cerevisiae MAF1 protein (GB:U19492) [Caenorhabditis elegans]	8.9
489	AF001000	Lycopersicon esculentum polygalacturonase 1	0.45	<NONE>	<NONE>	<NONE>
490	Z18920	Yersinia enterocolitica wbb gene cluster	0.41	<NONE>	<NONE>	<NONE>
491	D86983	Human mRNA for KIAA0230 gene, partial cds	0.35	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	4e-05
492	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.33	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes				
493	AF067083		0.33	401553	HYPOTHETICAL 24.5 KD PROTEIN IN NADB-SRMB INTERGENIC REGION	8.3
494	Y15520	Papio hamadryas anubis gene encoding fertilin alpha-II	0.29	2408049	(Z99164) hypothetical protein	3.1
495	U33475	Alestes sp. ependymin mRNA, partial cds	0.28	3913078	ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR HOMOLOG (DARNT) (TANGO PROTEIN) transcription factor [Drosophila melanogaster]	1.4
496	D88356	Mouse DNA for 8-oxodGTPase, complete cds	0.22	<NONE>	<NONE>	<NONE>
497	U67603	Methanococcus jannaschii section 145 of 150 of the complete genome	0.22	2209261	(U51222) p40 [Streptomyces halstedii]	8.3
498	U82386	Malurus cyaneus microsatellite McyU2	0.22	992631	(U29131) Mg-chelatase subunit [Synechocystis sp.]	0.56
499	Z49625	S.cerevisiae chromosome X reading frame ORF YJR125c	0.21	<NONE>	<NONE>	<NONE>
500	U64830	Dictyostelium discoideum AX2 protein tyrosine kinase gene, complete cds.	0.21	<NONE>	<NONE>	<NONE>
501	M24543	Human prostate-specific antigen (PA) gene, complete cds.	0.21	2764859	(X97918) gene 12.1 [Bacteriophage SPP1]	6.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					u0002b protein -	
502	X87618	B.taurus mRNA for thrombospondin (partial) 2162 bp	0.21	2146000	Mycobacterium tuberculosis tuberculosis] >gi\|1694863\|gnl\|PID\|e283373 (Z83018) hypothetical protein Rv2968c [Mycobacterium tuberculosis]	3.5
503	X71591	B.taurus microsatellite sequence INRA048	0.21	1354453	(U52830) orf [Homo sapiens]	2.7
504	X57808	Human germline immunoglobulin lambda light chain gene	0.21	2119158	procollagen type V alpha 2 - mouse >gi\|309181	2.7
505	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.21	2497139	HYPOTHETICAL 78.8 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION >gi\|1078003\|pir\|\|S52835 hypothetical protein YMR075w - yeast (Saccharomyces cerevisiae) >gi\|763022 (Z48952) unknown [Saccharomyces cerevisiae]	2.0
506	U84216	Mycobacterium fortuitum plasmid pJAZ38 replication protein Rep (rep) gene, complete cds	0.21	2499087	UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor [Drosophila melanogaster]	0.003
507	U31463	Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, complete cds.	0.21	3880111	(Z81130) predicted using Genefinder	0.002
508	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.21	630864	LRR47 protein - fruit fly (Drosophila melanogaster) >gi\|415947 (X75760) LRR47 [Drosophila melanogaster]	1e-06
509	AF086476	Homo sapiens full length insert cDNA clone ZD88F12	0.20	<NONE>	<NONE>	<NONE>
510	AF077006	Helicobacter pylori plasmid pHPM186, complete sequence	0.20	<NONE>	<NONE>	<NONE>
511	X75480	E.gunnii CAD gene.	0.20	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		T.aestivum				
512	X75036	mitochondrial nad7 gene for NADH dehydrogenase subunit 7	0.20	<NONE>	<NONE>	<NONE>
513	D90875	E.coli genomic DNA, Kohara clone #422(55.5-55.8 min.)	0.20	<NONE>	<NONE>	<NONE>
514	Z68343	Caenorhabditis elegans cosmid F59B8, complete sequence [Caenorhabditis elegans]	0.20	<NONE>	<NONE>	<NONE>
515	X62486	M.musculus V alpha 11.1 gene 5'-region	0.20	<NONE>	<NONE>	<NONE>
516	AF040651	Caenorhabditis elegans cosmid W04H10	0.20	1170683	PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, SKELETAL MUSCLE ISOFORM (PHOSPHORYLASE KINASE ALPHA M SUBUNIT) >gi\|2135923\|pir\|\|I38111 phosphorylase kinase (EC 2.7.1.38) - human >gi\|791043	7.4
517	U10470	Pseudomonas fluorescens PHA depolymerase (phaZ) gene, complete cds.	0.20	3721862	(AB016024) Pfj2 [Plasmodium falciparum]	1.9
518	D83778	Human mRNA for KIAA0194 gene, partial cds	0.20	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	0.65
519	S43579	c-scr=pp60c-src, sdr=src downstream region	0.20	4159887	(AC004908) similar to ribosomal protein L23a; similar to P29316 (PID:g132848) [Homo sapiens]	0.52
520	U07357	Mus musculus Balb/c brain-specific kinase (Bsk) mRNA, complete cds.	0.20	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	0.51

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
521	AF034460	Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.20	114136	AMINO-ACID ACETYLTRANSFERASE Pseudomonas aeruginosa >gi\|151036 (M38358) N-acetylglutamate synthase [Pseudomonas aeruginosa]	0.39
522	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.20	2842674	POU DOMAIN CLASS 2, ASSOCIATING FACTOR 1 (B-CELL-SPECIFIC COACTIVATOR OBF-1) (OCT BINDING FACTOR 1) (BOB-1) (OCA-B) Bob1, B-cell-specific - mouse >gi\|1881818\|bbs\|179852 mBob1=B-cell specific transcriptional coactivator line J558L, Peptide, 256 aa] >gi\|1353792 (U43788) Oct binding factor 1 [Mus musculus]	0.073
523	X95971	S.lividans groEL2 gene	0.20	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	4e-19
524	L41502	Ovis aries vasopressin V1 receptor (V1R) gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
525	J03885	K.pneumoniae oxalacetate decarboxylase alpha subunit gene, complete cds.	0.19	<NONE>	<NONE>	<NONE>
526	AE001451	Helicobacter pylori, strain J99 section 12 of 132 of the complete genome	0.19	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
527	D88084	Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)5'exon	0.19	<NONE>	<NONE>	<NONE>
528	U67599	Methanococcus jannaschii section 141 of 150 of the complete genome	0.19	<NONE>	<NONE>	<NONE>
529	J05500	Human beta-spectrin (SPTB) mRNA, complete cds.	0.19	<NONE>	<NONE>	<NONE>
530	Y10137	M.mycoides ftsY gene homologue and gene encoding hypothetical protein	0.19	<NONE>	<NONE>	<NONE>
531	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
532	D43805	Mouse thymic stromal cell mRNA for TLSF-beta, complete cds	0.19	<NONE>	<NONE>	<NONE>
533	AJ012585	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2	0.19	<NONE>	<NONE>	<NONE>
534	X51475	Brassica napus 5-enolpyruvylshikimate-3-phosphate synthase gene	0.19	<NONE>	<NONE>	<NONE>
535	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
536	Z49625	S.cerevisiae chromosome X reading frame ORF YJR125c	0.19	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens pilot				
537	X63741	mRNA	0.19	<NONE>	<NONE>	<NONE>
538	Y11255	O.latipes mRNA for annexin max4	0.19	<NONE>	<NONE>	<NONE>
539	L63537	Oncorhynchus mykiss (clone Jb-10) beta-2 microglobulin (B2m) mRNA, complete cds.	0.19	<NONE>	<NONE>	<NONE>
540	X70903	N.tobacum T92 gene for auxin-binding protein	0.19	<NONE>	<NONE>	<NONE>
541	U61958	Caenorhabditis elegans cosmid C25A8	0.19	<NONE>	<NONE>	<NONE>
542	U33959	Macaca fascicularis fertilin beta mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
543	Z49835	H.sapiens mRNA for protein disulfide isomerase	0.19	2113940	(Z95556) hypothetical protein Rv2507	9.4
544	AF035458	Spinacia oleracea heat shock 70 protein protein, complete cds	0.19	267293	PROBABLE E4 PROTEIN papillomavirus (type 1) >gi\|61015 (X62844) E4 gene product [Pygmy chimpanzee papillomavirus type 1]	9.4
545	U23441	Tetrahymena thermophila B internal deletion sequence.	0.19	3877185	(Z66563) F46C3.2 [Caenorhabditis elegans]	9.3
546	U53921	Pneumocystis carinii major surface glycoprotein	0.19	3548901	(AF052502) DA26 homolog [Epiphyas postvittana nucleopolyhedrovirus]	9.3
547	L11002	Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.19	3337352	(AC004481) putative chromatin structural protein Supt5hp	9.1
548	U67560	Methanococcus jannaschii section 102 of 150 of the complete genome	0.19	3183689	(Y13585) serotonin receptor 4 [Cavia porcellus]	8.7
549	U18424	Mus musculus bacteria binding macrophage receptor MARCO mRNA, complete cds.	0.19	3659853	(AF089083) complement component C1qB like protein	7.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U58751) C07G1.7 gene	
550	X66467	C.albicans sec18 gene	0.19	1326385	product [Caenorhabditis elegans]	6.9
551	AF003487	Syngaster lepidus 16S ribosomal RNA gene, partial sequence	0.19	3122039	DIHYDROPYRIMIDINASE (DHPASE) dihydropyrimidinase - rat >gi\|1378019\|gnl\|PID\|d1010479	6.9
552	J05087	Rat calmodulin-sensitive plasma membrane Ca2+-transporting ATPase (PMCA3) mRNA, complete cds.	0.19	422462	hypothetical protein - fruit fly (Drosophila melanogaster) >gi\|296434 (X68408) ORF [Drosophila melanogaster]	5.3
553	AF080464	Homo sapiens glutamate oxaloacetate transaminase	0.19	3024834	PROBABLE E4 PROTEIN >gi\|790898 position 3286..3288 is first start codon; putative	5.3
554	U78876	Human MEK kinase 3 mRNA, complete cds	0.19	1710445	(U78083) unknown [Emericella nidulans]	5.3
555	AB009077	Vigna radiata mRNA for proton pyrophosphatase, complete cds	0.19	3256922	(AP000002) 256aa long hypothetical protein [Pyrococcus horikoshii]	5.1
556	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.19	4226159	(AF125463) contains similarity to BTB (also known as BR-C/Ttk) domains (Pfam:PF00651, Score=62.8, E=7.6e-15, N=1) [Caenorhabditis elegans]	4.1
557	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
558	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.0
559	L81774	Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence	0.19	4001725	(AB015981) MnhA [Staphylococcus aureus]	3.0
560	AL021108	Drosophila melanogaster cosmid clone 137E7	0.19	4001688	(AB015718) protein kinase [Homo sapiens]	3.0
561	AB001510	Carabus leptoplesioides mitochondrial DNA for NADH dehydrogenase subunit 5, partial cds	0.19	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	2.4
562	AF069696	Egernia stokesii clone EST1 microsatellite	0.19	3328994	(AE001326) Amino Acid (Branched) Transport [Chlamydia trachomatis]	2.4
563	X64144	F.pringlei ppcA1 gene for phosphoenolpyruvate carboxylase	0.19	3242974	(AF069555) G protein-coupled receptor p2y3 [Meleagris gallopavo]	2.3
564	U56897	Human immunodeficiency virus type 1 gag polyprotein (gag) gene, partial cds	0.19	2257710	(U73041) resolvase-like protein [Thiobacillus ferrooxidans]	2.3
565	U57975	Danio rerio Notch homologue 3 mRNA, complete cds	0.19	3874971	(Z99709) similar to NAD dependant epimerase/dehydratase family; cDNA EST EMBL:C10103 comes from this gene; cDNA EST EMBL:D66400 comes from this gene; cDNA EST EMBL:D70143 comes from this gene; cDNA EST yk493h11.3 comes from ...	1.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					masquerade precursor - fruit fly	
566	Y12502	R.norvegicus mRNA for factor XIIIa	0.19	2133693	(Drosophila melanogaster) >gi\|665545 (U18130) masquerade [Drosophila melanogaster] >gi\|1095942\|prf\|\|2110286A masquerade gene	1.8
567	S82470	BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	0.19	2444026	(U77783) N-methyl-D-aspartate receptor 2D subunit precursor [Homo sapiens]	1.8
568	U97408	Caenorhabditis elegans cosmid F48A9	0.19	542433	225K protein - Babesia bovis (fragment)	1.8
569	U10470	Pseudomonas fluorescens PHA depolymerase (phaZ) gene, complete cds.	0.19	3721862	(AB016024) Pfj2 [Plasmodium falciparum]	1.7
570	M88160	Ovis aries MAF214 locus polymorphic dinucleotide repeat .	0.19	1293816	(U56963) T13A10.5 gene product [Caenorhabditis elegans]	1.4
571	AJ131336	Holcus lanatus mRNA for pollen allergen (Hol l 2, group II) > :: emb\|AJ131339\|LIT13 1339 Lolium italicum mRNA for pollen allergen (Lol i 2, group II) > allergen (Poa p 2, group II) > :: emb\|AJ131338\|TAE1 31338 Triticum aestivum mRNA for pollen allergen (Tri a 2, group II)	0.19	3880447	(AL032675) predicted using Genefinder	0.82
572	X84036	S.cerevisiae ARG8 and CDC33 genes	0.19	3882041	(AJ010405) hypothetical protein	0.62

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human WD protein			mucin - human >gi\|501033	
573	U57058	IR10 pre-mRNA, partial cds	0.19	631302	(U14383) mucin [Homo sapiens]	0.60
574	AF034460	Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.19	114136	AMINO-ACID ACETYLTRANSFERASE Pseudomonas aeruginosa >gi\|151036 (M38358) N-acetylglutamate synthase [Pseudomonas aeruginosa]	0.35
575	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.19	105270	alpha-2-adrenergic receptor - human name 'ADRA2R' [Homo sapiens]	0.27
576	AG001475	Homo sapiens genomic DNA, 21q region, clone: 125H6N2	0.19	94977	hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pKB740 >gi\|45867 (X66604) ORF3	0.16
577	M63284	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 9 and 10, clones lambda-Fc(3.2,93).	0.19	3024681	TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) of RNA polymerase II transcription factor TFIID [Homo sapiens]	0.088
578	U38241	Pseudomonas aeruginosa orotate phophoribosyl transferase (pyrE), catabolite repression control protein (crc) and RNasePH (rph) genes, complete cds	0.19	3044086	(AF055904) unknown [Myxococcus xanthus]	0.052
579	AF039734	Lontra longicaudis transthyretin intron 1, partial sequence	0.19	322759	pistil extensin-like protein (clone pMG14) - common tobacco (fragment) >gi\|19927 (Z14015) pistil extensin like protein [Nicotiana tabacum]	0.030
580	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.19	2147194	collagen - Paralvinella grasslei	0.002

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
581	AB004232	Drosophila melanogaster mRNA for DAD polypeptide, complete cds	0.19	2498765	PEROXISOMAL MEMBRANE PROTEIN PEX16 lipolytica]	0.002
582	AF098919	Gallus gallus alpha-globin gene domain 5' region	0.19	1086863	(U41272) T03G11.6 gene product [Caenorhabditis elegans]	4e-05
583	AE001457	Helicobacter pylori, strain J99 section 18 of 132 of the complete genome	0.19	2924552	(AL022018) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=165.48; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA264666; 2-match_description=LD08351.5prime LD Drosophila melanoga...	3e-05
584	L10329	Plasmid RP4 traE gene, 3' end; traD gene, complete cds; traF gene, 5' end.	0.19	3878117	(Z49068) mitochondrial carrier protein	8e-07
585	AE001155	Borrelia burgdorferi (section 41 of 70) of the complete genome	0.19	861276	(U28739) similar to TPR domains in e.g. yeast STI1 protein [Caenorhabditis elegans]	2e-12
586	U49979	Orf virus E10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.19	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	1e-15
587	U88155	Xenopus laevis RanGTPase activating protein	0.19	995714	(X91258) pid:e198503 [Saccharomyces cerevisiae]	4e-16
588	AF061854	Schizosaccharomyces pombe Clr4p (clr4) gene, complete cds	0.19	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-19
589	M23865	S.cerevisiae CHS2 gene encoding chitin synthase.	0.18	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis XL-				
590	U95094	INCENP (XL-INCENP) mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
591	AF067610	Caenorhabditis elegans cosmid F41A4	0.18	<NONE>	<NONE>	<NONE>
592	AF036329	Homo sapiens gonadotropin-releasing hormone precursor, second form (GnRH-II) gene, complete cds	0.18	<NONE>	<NONE>	<NONE>
593	Z49216	H.sapiens mitoxantrone-resistance associated mRNA	0.18	<NONE>	<NONE>	<NONE>
594	X02167	Torulopsis glabrata mitochondrial DNA for tRNA-Thr,-His and -Glu upstream of cytochrome b gene	0.18	<NONE>	<NONE>	<NONE>
595	Z31561	R.communis (Carmencita) Scr1 mRNA for sucrose carrier	0.18	<NONE>	<NONE>	<NONE>
596	L81692	Homo sapiens (subclone 2_c9 from P1 H56) DNA sequence	0.18	1346575	55 KD ERYTHROCYTE MEMBRANE PROTEIN	8.4
597	X57310	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L-cysteinyl-D-valine synthetase and isopenicillin N synthase	0.18	126404	SEED LIPOXYGENASE-2 (L-2) soybean >gi\|170014 (J03211) lipoxygenase (EC 1.13.11.12)	6.5
598	U18315	Sus scrofa parathyroid receptor (PTH) mRNA, complete cds	0.18	1022323	(X04647) collagen alpha-2(IV) chain [Mus musculus]	3.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
599	AL010158	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-85, complete sequence	0.18	2506816	VERSICAN CORE PROTEIN PRECURSOR PROTEOGLYCAN CORE PROTEIN 2) (GLIAL HYALURONATE-BINDING PROTEIN) (GHAP) >gi\|608515 (U16306) chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide	3.7
600	AB005287	Bos taurus mRNA for thrombospondin 1, complete cds	0.18	2146000	u0002b protein - Mycobacterium tuberculosis tuberculosis] >gi\|1694863\|gnl\|PID\|e283373 (Z83018) hypothetical protein Rv2968c [Mycobacterium tuberculosis]	2.9
601	AL021108	Drosophila melanogaster cosmid clone 137E7	0.18	3483032	(AL031371) hypothetical protein SC4G2.06 [Streptomyces coelicolor]	2.9
602	U57975	Danio rerio Notch homologue 3 mRNA, complete cds	0.18	85719	collagen alpha 1'(II) chain precursor - African clawed frog	1.7
603	M30124	P.aeruginosa autonomously replicating sequence.	0.18	3878017	(AL021387) similar to Zinc finger, C4 type (two domains); cDNA EST yk452f4.5 comes from this gene; cDNA EST EMBL:T00774 comes from this gene receptor NHR-3 [Caenorhabditis elegans]	1.3
604	X54965	G.sp alpha 5HR DNA	0.18	134304	STEM CELL PROTEIN chicken >gi\|62845 (X63371) transforming capacity [Gallus gallus]	1.3
605	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.18	1628403	(X98893) hTAFII68 [Homo sapiens] splicing [Homo sapiens]	1.3
606	U20793	Oryctolagus cuniculus renal sodium-dependent phosphate transporter type II mRNA, complete cds.	0.18	1705984	92 KD TYPE IV COLLAGENASE PRECURSOR IV, 92K, precursor - rat >gi\|1022784 (U36476) 92-kDa type IV collagenase [Rattus norvegicus]	1.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
607	U23427	Human cholecystokinin type A receptor (CCK-A) gene, exons 1 and 2.	0.18	3261734	(Z94752) hypothetical protein Rv1004c	0.97
608	U49953	Rattus norvegicus protein kinase MUK2 mRNA, complete cds	0.18	551238	(X81847) pectate lyase 1 [Erwinia carotovora]	0.43
609	J00182	Human alpha globin gene cluster on chromosome 16: zeta gene.	0.18	1585259	traJ gene [Amycolatopsis methanolica]	0.41
610	X62513	M.gallopavo gene for metallothionein	0.18	2494740	HYPOTHETICAL 28.3 KD PROTEIN IN GBD 5'REGION (ORF4) >gi\|2120954\|pir\|\|I39562 ORF4 - Alcaligenes eutrophus >gi\|695274 (L36817) ORF4	0.31
611	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.18	86837	androgen receptor B - human	0.082
612	M12450	Rat vitamin D binding protein (DBP) mRNA, complete cds.	0.18	4210432	(AJ130783) APC2 protein [Mus musculus]	0.038
613	AF038539	Mus musculus muscle NSP-like 1 (Nspl1) mRNA, complete cds	0.18	3297877	(AJ224868) GNAS1 [Homo sapiens]	0.029
614	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.18	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.009
615	D38754	Pig mRNA for inter-alpha-trypsin inhibitor heavy-chain H1, complete cds	0.18	1397275	(U61947) C06G3.8 gene product [Caenorhabditis elegans]	7e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					LRR47 protein - fruit fly	
616	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.18	630864	(Drosophila melanogaster) >gi\|415947 (X75760) LRR47 [Drosophila melanogaster]	6e-07
617	X54850	S.kluyveri linear plasmid pSKL DNA for open reading frames 1-10	0.18	3183405	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi\|2370504\|gnl\|PID\|e339194 pombe] >gi\|3451305\|gnl\|PID\|e1316730 (AL031324) very hypothetical protein [Schizosaccharomyces pombe]	2e-08
618	L21954	Human peripheral benzodiazepine receptor gene, exon 4.	0.18	3925211	(AL032626) cDNA EST EMBL:D70654 comes from this gene; cDNA EST EMBL:Z14359 comes from this gene; cDNA EST EMBL:D33409 comes from this gene; cDNA EST EMBL:D36239 comes from this gene; cDNA EST EMBL:Z14766 comes from this gene...	4e-09
619	U09355	Oryctolagus cuniculus protein phosphatase 2A1 B gamma subunit (skeletal muscle isolate) mRNA, complete cds.	0.18	3947877	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]	8e-11
620	X58715	T.cruzi hsp70 mRNA for 70 kDa heat shock protein, partial cds	0.18	3024081	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) (CONTAINS: TELOKIN)	9e-12
621	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	0.18	861276	(U28739) similar to TPR domains in e.g. yeast STI1 protein [Caenorhabditis elegans]	1e-14
622	L27235	Methylobacterium extorquens serine cycle proteins	0.18	2688949	(AF027208) AC133 antigen [Homo sapiens]	1e-14

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
623	AF006573	Drosophila virilis maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.18	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi\|3876420\|gnl\|PID\|e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-23
624	AF001782	Staphylococcus aureus strain SA502A AgrB	0.17	<NONE>	<NONE>	<NONE>
625	AJ223364	Homo sapiens germ-line DNA upstream of Jkappa locus	0.17	<NONE>	<NONE>	<NONE>
626	J03059	Human glucocerebrosidase (GCB) gene, complete cds	0.17	<NONE>	<NONE>	<NONE>
627	AB008860	Fugu rubripes Ca12 gene for pheromone receptor, complete cds	0.17	2198849	(AF004900) E3KARP [Homo sapiens] >gi\|2665826 (AF035771) Na+/H+ exchanger regulatory factor 2 [Homo sapiens] factor 2 [Homo sapiens] >gi\|3618353\|gnl\|PID\|d1034182 exchanger isoform A3 [Homo sapiens]	7.8
628	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.17	539355	SCD25 protein (version 1) - yeast	7.5
629	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	482118	hypothetical protein C15H7.1 - Caenorhabditis elegans	4.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
630	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	465932	~~HYPOTHETICAL 83.2 KD~~ PROTEIN F58A4.11 IN CHROMOSOME III >gi\|3874287\|gnl\|PID\|e1344088 EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ... EMBL:C11886 comes from this gene; cDNA EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ...	4.4
631	X55065	Chinese hamster metallothionein II gene	0.17	3687237	(AC005169) putative Cys3His zinc-finger protein	1.5
632	U15280	Rattus norvegicus oxytocin receptor (OTR) gene, exon 3 and complete cds	0.17	542565	cyclin E type II - fruit fly (Drosophila melanogaster) >gi\|429168 (X75027) Drosophila cyclin E type II [Drosophila melanogaster]	0.45
633	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.17	86837	androgen receptor B - human	0.080
634	AL010222	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence	0.17	1177322	(X95466) CPG2 protein [Rattus norvegicus] >gi\|1588593\|prf\|\|2208498A plasticity-related gene [Rattus norvegicus]	7e-07
635	X60111	H.sapiens mRNA for MRP-1	0.17	3237306	(U92715) breast cancer antiestrogen resistance 3 protein	3e-09
636	U49979	Orf virus E10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.17	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	7e-15

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
637	AF006573	Drosophila virilis maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.17	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi\|3876420\|gnl\|PID\|e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-29
638	AE001141	Borrelia burgdorferi (section 27 of 70) of the complete genome	0.16	1850327	(U52370) fertilin beta [Homo sapiens]	2.3
639	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.12	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	2e-56
640	AF023532	Simulium vittatum ATPase 6 gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.11	<NONE>	<NONE>	<NONE>
641	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.10	3482965	(AL031369) putative protein	0.49
642	AJ001596	Danio rerio mRNA for opioid receptor homologue	0.099	1706694	LANOSTEROL SYNTHASE 5.4.99.7) - fission yeast (Schizosaccharomyces pombe)	2.3
643	U26341	Oryctolagus cuniculus Na and Cl dependent betaine transporter mRNA, complete cds.	0.099	2645804	(AF033381) betaine homocysteine methyl transferase [Mus musculus]	0.59
644	M11633	Bacteriophage Cp-5 (S.pneumoniae) 3' inverted terminal repeat.	0.082	2314695	(AE000649) type IIS restriction enzyme R and M protein	4.3
645	X74103	Streptomyces sp. gene for alkaline serine protease I	0.073	1314734	(U54641) 220 kDa silk protein [Chironomus thummi]	6.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
646	Z72509	elegans cosmid F32G8, complete sequence [Caenorhabditis elegans]	0.072	<NONE>	<NONE>	<NONE>
647	X70282	X.laevis xanf-1 gene	0.070	3851202	(AC005954) ZO-3 [Homo sapiens] [Homo sapiens]	0.40
648	Z69906	Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.069	<NONE>	<NONE>	<NONE>
649	AF056940	Drosophila virilis retrotransposon Tv1, complete sequence	0.069	2246532	(U93872) ORF 73, contains large complex repeat CR 73	5e-12
650	AJ001151	Homo sapiens genomic sequence	0.068	<NONE>	<NONE>	<NONE>
651	X54455	Bacteriophage BF23 gene 17 and gene 18	0.067	<NONE>	<NONE>	<NONE>
652	X87936	P.pinea internal transcribed spacers 1 & 2 of ribosomal DNA	0.067	2459733	(U95374) aldehyde dehydrogenase [Haloferax volcanii]	4.3
653	AF019236	Dictyostelium discoideum TipD (tipD) gene, complete cds	0.067	3882275	(AB018320) KIAA0777 protein [Homo sapiens]	1.1
654	X90592	O.cuniculus mRNA for p53 protein	0.067	1703275	METHIONINE AMINOPEPTIDASE 2 (METAP 2) GLYCOPROTEIN) (P67)	0.29
655	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor mRNA, partial cds	0.067	642518	(U17326) neuronal nitric oxide synthase [Homo sapiens]	0.29
656	AB007881	Homo sapiens KIAA0421 mRNA, partial cds	0.066	<NONE>	<NONE>	<NONE>
657	AL010213	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-109, complete sequence	0.066	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
658	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.066	1082461	homeotic protein HB9 - human	0.38
659	AF104156	Rattus exulans isolate huahine30 mitochondrial D-loop, partial sequence	0.066	1002380	(U24189) RRM-type RNA binding protein [Caenorhabditis elegans]	0.29
660	X97581	M.musculus mRNA for spalt transcription factor	0.066	4107313	(AL035075) putative myosin heavy chain	0.28
661	D85378	Human clone H20 N-acetylglucosaminyltransferase III DNA, exon 2	0.066	2114473	(U96963) p140mDia [Mus musculus]	0.22
662	M97561	Human (clone LA179) chromosome 21 sequence.	0.065	<NONE>	<NONE>	<NONE>
663	AE001373	Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence	0.065	<NONE>	<NONE>	<NONE>
664	S75479	growth hormone receptor, growth hormone binding protein {GHR/BP gene} [mice, C57 black/6, Genomic, 179 nt, segment 8 of 10]	0.065	<NONE>	<NONE>	<NONE>
665	AF032922	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds	0.065	3061308	(AB006074) topoisomerase III [Mus musculus]	0.82
666	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	0.065	1326288	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.12

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 74.2 KD	
667	X59552	G.domesticus mRNA for ventricular myosin heavy chain	0.065	2497098	PROTEIN IN AMD1-RAD52 INTERGENIC REGION >gi\|1077180\|pir\|\|S49745 probable membrane protein YML034w - yeast (Saccharomyces cerevisiae) >gi\|575685 (Z46659) unknown orf, len: 656, CAI: 0.13 [Saccharomyces cerevisiae]	0.014
668	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.065	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-33
669	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
670	M30039	Sheeppox virus strain KS-1 ORF HM1 gene, partial cds; ORF HM2 and ORF HM3 genes, complete cds; and ORF HM4 gene, partial cds	0.064	<NONE>	<NONE>	<NONE>
671	Z68013	Caenorhabditis elegans cosmid W02H3, complete sequence [Caenorhabditis elegans]	0.064	<NONE>	<NONE>	<NONE>
672	AF041332	Bodo saltans unknown mRNA, kinetoplast gene encoding kinetoplast protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
673	J00451	Mouse germline IgG-3 chain gene, D-J-C region, and switch region.	0.064	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
674	U41289	Dictyostelium discoideum K7 kinesin-like protein mRNA, complete cds	0.064	3482972	(AL031369) putative protein	9.3
675	M37395	L.lactis (strain SK11) proteinase plasmid pSK111 DNA, complete cds.	0.064	993019	(X87246) alternative start codon [Pseudorabies virus]	9.2
676	Z15030	H.sapiens gene for ventricular myosin light chain 2 > :: gb\|L01652\|HUMVM LC Human ventricular myosin light chain 2 gene, seven exons.	0.064	730343	PROLACTIN RECEPTOR PRECURSOR (PRL-R) mouse >gi\|220576\|gnl\|PID\|d1001535 (D10214) prolactin receptor precursor [Mus musculus] >gi\|293770 (L14811) prolactin receptor [Mus musculus] >gi\|347842 (L13593) prolactin receptor [Mus musculus] receptor:ISOTYPE=long form [Mus musculus]	9.1
677	Z12021	G.max gene for catalase	0.064	2498711	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi\|1185461 (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe]	5.3
678	L05668	Entamoeba histolytica protein serine/threonine kinase (pstk1) gene, complete cds.	0.064	733140	(U22453) carboxypeptidase [Simulium vittatum]	5.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
679	U50715	Mus musculus alpha-galactosidase A gene, complete cds	0.064	125398	HYGROMYCIN-B KINASE (HYGROMYCIN B PHOSPHOTRANSFERASE) (APH(7")) >gi\|66885\|pir\|\|WGSMHH hygromycin B phosphotransferase (EC 2.7.1.-) - Streptomyces hygroscopicus >gi\|581682 (X03615) pot. hyg protein [Streptomyces hygroscopicus] phosphotransferase [synthetic construct] >gi\|2739064 cloning vector] >gi\|2739068 (AF025747) hygromycin B phosphotransferase [unidentified cloning vector]	2.3
680	Z28182	S.cerevisiae chromosome XI reading frame ORF YKL182w	0.064	1079035	Om(2D) protein - fruit fly (Drosophila ananassae) >gi\|443770\|gnl\|PID\|d1006095 (D26553) ORF	1.8
681	M29917	Human ornithine aminotransferase gene, exon 1.	0.064	2317934	(U97553) unknown [murine herpesvirus 68]	1.4
682	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.064	861404	(U29154) T07F12.3 gene product [Caenorhabditis elegans]	0.47
683	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	1708118	HOMEOBOX PROTEIN HB9 >gi\|507425	0.35
684	AB010427	Homo sapiens mRNA for NORI-1, complete cds	0.064	2388676	(AF015539) precollagen P [Mytilus edulis]	0.018
685	U34774	Orf virus ankyrin-like repeat protein, F11L homolog, and F12L homolog genes, complete cds.	0.064	731668	SSF1 PROTEIN >gi\|626624\|pir\|\|S46700 SSF1 protein - yeast (Saccharomyces cerevisiae)	1e-05
686	AF022861	Mus musculus neuropilin-2(a5) mRNA, alternatively spliced, complete cds	0.064	4091978	(AF073359) benzaldehyde dehydrogenase [Pseudomonas sp. DJ77]	1e-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC004010) similar to Leucine-	
687	U14331	Sus scrofa myogenin gene, complete cds	0.064	2781386	rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	3e-33
688	AF074870	Chironomus pallidivittatus clone 1219 non-telomeric Ssp repeat sequence	0.063	<NONE>	<NONE>	<NONE>
689	Z25523	H.sapiens repeat region DNA.	0.063	<NONE>	<NONE>	<NONE>
690	AE001378	Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence	0.063	<NONE>	<NONE>	<NONE>
691	Z72947	S.cerevisiae chromosome VII reading frame ORF YGR162w	0.063	<NONE>	<NONE>	<NONE>
692	Y14723	Choanomphalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.063	<NONE>	<NONE>	<NONE>
693	X74103	Streptomyces sp. gene for alkaline serine protease I	0.063	1730713	HYPOTHETICAL 108.5 KD PROTEIN IN UME3-PUB1 INTERGENIC REGION >gi\|2131866\|pir\|\|S62935 hypothetical protein YNL023c - yeast (Saccharomyces cerevisiae) >gi\|1301855\|gnl\|PID\|e239870 (Z71299) ORF YNL023c [Saccharomyces cerevisiae]	6.7
694	AF039843	Homo sapiens Sprouty 2 (SPRY2) mRNA, complete cds	0.063	232217	GLUTATHIONE S-TRANSFERASE GST-6.0 (GST B1-1) >gi\|421198\|pir\|\|S29772 glutathione transferase (EC 2.5.1.18) - Proteus mirabilis >gi\|2126142\|pir\|\|S71882 glutathione transferase (EC 2.5.1.18) B - Proteus mirabilis >gi\|1053076 (U38482)	5.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
695	M63650	Mouse M-twist gene mRNA, complete cds.	0.063	1730141	FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 2 >gi\|2135129\|pir\|\|S60173 fragile X mental retardation syndrome related protein - human >gi\|1098637 (U31501) fragile X mental retardation syndrome related protein [Homo sapiens]	1.8
696	Y13298	Homo sapiens GDP dissociation inhibitor beta pseudogene	0.063.	1085930	hypothetical protein 4 - fowl adenovirus 1	1.3
697	X56600	Rat SOD-2 gene for manganese-containing superoxide dismutase	0.063	3882143	(AB018254) KIAA0711 protein [Homo sapiens]	0.60
698	Z23107	M.musculus mRNA for 5HTx serotonin receptor	0.063	1708162	HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN HOMOLOG) (HD PROTEIN)	0.45
699	M20670	Plasmodium vivax circumsporozoite protein gene, 3' end.	0.063	4033395	DNA GYRASE SUBUNIT B subunit [Myxococcus xanthus]	0.35
700	Z62997	H.sapiens CpG DNA, clone 76g11, reverse read cpg76g11.rt1a .	0.063	1350911	RETINOIC ACID RECEPTOR RXR-BETA sapiens] >gi\|3172498 (AF065396) retinoic X receptor B dJ1033B10.11 (Retinoid X receptor beta (RXRB)) [Homo sapiens] >gi\|4249766 (AF120161) retinoic X receptor beta	0.16
701	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.063	2981200	(AF048732) cyclin T2b [Homo sapiens]	0.090
702	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.063	3877951	(Z81555) predicted using Genefinder	6e-07
703	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.063	3393018	(AL031174) hypothetical protein	2e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		E.coli genomic DNA,				
704	D90872	Kohara clone #419(54.7-55.1 min.)	0.063	2498198	CYTOCHROME B561 (CYTOCHROME B-561)	3e-19
705	M25528	M.crystallinum ferredoxin-NADP+ reductase (fnrA) mRNA, complete cds.	0.062	<NONE>	<NONE>	<NONE>
706	U45256	Strongyloides ratti microsatellite B DNA	0.062	<NONE>	<NONE>	<NONE>
707	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.062	<NONE>	<NONE>	<NONE>
708	AF044317	Homo sapiens TEL/AML1 fusion gene, partial sequence	0.062	<NONE>	<NONE>	<NONE>
709	Z73975	Caenorhabditis elegans cosmid T06E8, complete sequence [Caenorhabditis elegans]	0.062	3108187	(AC004663) Notch 3 [Homo sapiens]	2.9
710	X54232	Human mRNA for heparan sulfate proteaglycan	0.062	1076741	chitinase (EC 3.2.1.14) precursor - rice precursor - rice >gi\|807955 (X87109) chitinase [Oryza sativa]	0.59
711	X03073	Bovine retinal mRNA for transducin beta-subunit	0.062	477578	sialidase - Actinomyces viscosus >gi\|141852	0.087
712	Y12573	D.melanogaster Jun and 14-3-3 zeta gene	0.062	3879551	(Z70756) similar to collagen	0.073
713	L26573	Bombus terrestris mitochondrial cytochrome oxidase I, partial cds.	0.062	1684959	(U20600) NADH dehydrogenase subunit [Vanda lamellata]	0.039

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					AMINOPEPTIDASE B	
714	U58994	Human ladinin (LAD) gene, complete cds	0.062	2811078	(ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B) >gi\|2039143 (U61696) aminopeptidase B [Rattus norvegicus]	9e-06
715	AB014553	Homo sapiens mRNA for KIAA0653 protein, partial cds	0.062	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nulcear division RFT1 protein (SP:P38206)	5e-10
716	L16898	Mus musculus collagen alpha 1 type XVIII mRNA, 5'end.	0.062	1723657	HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi\|2132587\|pir\|\|S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi\|1323010\|gnl\|PID\|e243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	1e-14
717	X99343	M.tuberculosis guaA/B & choD genes	0.062	3873807	(Z49907) B0491.1 [Caenorhabditis elegans]	2e-19
718	AF010193	Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds	0.061	<NONE>	<NONE>	<NONE>
719	L10182	Myrmeleon sp. 18S ribosomal RNA.	0.061	<NONE>	<NONE>	<NONE>
720	Y14723	Choanomphalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.061	<NONE>	<NONE>	<NONE>
721	L27840	Bovine respiratory syncytial virus nucleoprotein mRNA, complete cds.	0.061	542955	nucleoporin p62 - human	8.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					Sus scrofa	
722	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.061	494454	>gi\|494455\|pdb\|1POS\|B Sus scrofa Sus scrofa >gi\|1421210\|pdb\|1PCP\| Porcine Spasmolytic Protein (Psp) (Nmr, 19 Structures) Spasmolytic Polypeptide >gi\|1633061\|pdb\|2PSP\|B Chain B, Porcine Pancreatic Spasmolytic Polypeptide	2.9
723	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.061	3845272	(AE001417) hypothetical protein [Plasmodium falciparum]	1.3
724	U26463	Sporidiobolus salmonicolor NADPH-dependent aldehyde reductase gene, complete cds	0.061	1710288	(U79302) unknown [Homo sapiens]	0.44
725	AF035443	Xenopus laevis wee1 homolog mRNA, complete cds	0.061	3979720	(Z50109) cDNA EST EMBL:D33048 comes from this gene; cDNA EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E... >gi\|3979816\|gnl\|PID\|e1358315 EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E...	2e-04
726	Z48584	Caenorhabditis elegans cosmid ZK1321, complete sequence [Caenorhabditis elegans]	0.061	3183491	HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III >gi\|1065510 (U40419) C27F2.7 gene product [Caenorhabditis elegans]	3e-11

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 32.0 KD	
727	X61489	Zea mays pep gene for (C3 type) phosphoenolpyruvate carboxylase	0.061	2496887	PROTEIN C09F5.2 IN CHROMOSOME III >gi\|732538 (U22832) C09F5.2 gene product [Caenorhabditis elegans]	1e-15
728	AF025408	Drosophila melanogaster Windbeutel (wind) gene, complete cds	0.061	3702295	(AC005783) R33083_1 [Homo sapiens]	2e-60
729	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.060	<NONE>	<NONE>	<NONE>
730	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
731	Y08682	H.sapiens mRNA for carnitine palmitoyltransferase I type I	0.060	3319446	(AF077541) contains similarity to class-I aminoacyl-tRNA synthetases [Caenorhabditis elegans]	8.1
732	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.060	1041119	(D78016) TRAE [Enterococcus faecalis]	8.1
733	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.060	632209	regulatory protein Rex - primate T-lymphotropic virus PTLV-L (fragment)	3.7
734	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.060	3098348	(AF037401) neuropeptide Y/peptide YY receptor Yc [Danio rerio]	2.1
735	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.060	125978	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) >gi\|70146\|pir\|\|TDHULK leukocyte antigen-related protein precursor - human >gi\|34267 sapiens]	1.2
736	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.060	2055394	(U87306) transmembrane receptor UNC5H2 [Rattus norvegicus]	0.32
737	U69668	Human nuclear pore complex-associated protein TPR	0.060	4127854	(Y14063) ChT1 thymocyte antigen [Gallus gallus]	9e-04

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U58748) similar to potential	
738	AB014553	Homo sapiens mRNA for KIAA0653 protein, partial cds	0.060	1326350	transmembrane domains in S. cerevisiae nulcear division RFT1 protein (SP:P38206)	1e-09
739	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.060	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	5e-10
740	Z96260	H.sapiens telomeric DNA sequence, clone 12QTEL101, read 12QTELOO101.seq	0.059	<NONE>	<NONE>	<NONE>
741	M93128	Mouse homeobox protein (EVX2) mRNA, complete cds.	0.059	<NONE>	<NONE>	<NONE>
742	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.059	1652318	(D90904) lysostaphin [Synechocystis sp.]	4.7
743	AB007920	Homo sapiens mRNA for KIAA0451 protein, complete cds	0.059	479491	transcription factor brn-3b - human	0.71
744	M60445	Human histidine decarboxylase (HDC) mRNA, complete cds	0.058	<NONE>	<NONE>	<NONE>
745	U01836	Ustilago maydis exodeoxyribonucleas e (REC1) gene, complete cds.	0.058	1171908	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC >gi\|1075086\|pir\|\|D64184 oligopeptide transport system permease protein (oppC)C homolog - Haemophilus influenzae (strain Rd KW20) permease protein (oppC) [Haemophilus influenzae Rd]	1.5
746	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.058	3193265	(AF069131) chitinase [Bacillus subtilis]	0.002
747	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.057	433385	(U03978) dynein heavy chain isotype 7A [Tripneustes gratilla]	3.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana				
748	AJ005813	mRNA for neoxanthin cleavage enzyme	0.056	<NONE>	<NONE>	<NONE>
749	Y16828	Lagopus lagopus genomic microsatellite sequence, LLST4	0.056	3328678	(AE001299) hypothetical protein [Chlamydia trachomatis]	4.3
750	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.055	<NONE>	<NONE>	<NONE>
751	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.055	137339	69 KD PROTEIN >gi\|94375\|pir\|\|S19150 hypothetical protein, 69K - turnip yellow mosaic virus	0.69
752	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.035	<NONE>	<NONE>	<NONE>
753	M92069	Human retrovirus-like sequence-isoleucine c	0.034	<NONE>	<NONE>	<NONE>
754	S78516	G1L=ankyrin-like repeat [orf virus OV, NZ2, Genomic, 1608 nt]	0.033	2804465	(AF043700) contains similarity to human RNA-binding protein FUS/TLS (SW:Q28009) [Caenorhabditis elegans]	0.15
755	M15646	Chicken myosin alkali light chain mRNA, complete cds, clone pF1.	0.027	3334221	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]	6e-17
756	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.025	3877815	(Z96048) predicted using Genefinder	5.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
757	AJ002291	Streptococcus pneumoniae pbp1b gene, complete	0.025	3880487	(Z68014) similar to ribose-phosphate pyrophosphokinase; cDNA EST EMBL:D73173 comes from this gene; cDNA EST EMBL:D70909 comes from this gene; cDNA EST EMBL:D73449 comes from this gene; cDNA EST EMBL:D76167 comes from this ge...	1.7
758	X79104	C.botulinum (NCTC 7272 type A) HA-33 and P-21 genes.	0.024	2648615	(AE000970) tungsten formylmethanofuran dehydrogenase, subunit B (fwdB 2) [Archaeoglobus fulgidus]	6.1
759	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.024	1663698	(D83785) expressed ubiquitously; product similar to D.melanogaster mam protein. [Homo sapiens]	4.7
760	U36197	Chlamydomonas reinhardtii cobalamin-independent methionine synthase mRNA, complete cds	0.024	585723	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA) >gi\|283818\|pir\|\|C42214 peroxisome proliferator-activated receptor gamma chain - African clawed frog >gi\|214668 (M84163) peroxisome proliferator activated receptor gamma [Xenopus laevis]	0.42
761	L38865	Macaca mulatta (clone MMVA63) T-cell receptor alpha (TCR A) mRNA, partial cds.	0.023	<NONE>	<NONE>	<NONE>
762	AF035948	Mus musculus insulin receptor substrate-3	0.023	2500587	SPLICEOSOME ASSOCIATED PROTEIN 49 spliceosome-associated protein SAP-49 - human >gi\|556217	0.40
763	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.023	110072	proline-rich protein MP4 - mouse >gi\|53182	0.18

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
764	X91212	L.esculentum mRNA for HD-ZIP protein	0.022	<NONE>	<NONE>	<NONE>
765	AC004498	Homo sapiens chromosome 5, P1 clone 1209C1 (LBNL H104), complete sequence [Homo sapiens]	0.022	<NONE>	<NONE>	<NONE>
766	U07083	Human prostatic acid phosphatase (ACPP) gene, exon 1	0.022	<NONE>	<NONE>	<NONE>
767	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.022	<NONE>	<NONE>	<NONE>
768	X56488	L.esculentum LAT59 gene 5'flanking region, expressed during pollen maturation	0.022	<NONE>	<NONE>	<NONE>
769	M34651	Pseudorabies virus with upstream and downsteam sequences.	0.022	<NONE>	<NONE>	<NONE>
770	X66727	P.taeda gene for protochlorophyllide reductase	0.022	3878517	(Z92806) K10G4.4 [Caenorhabditis elegans]	4.3
771	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.022	1854452	(D89501) similar to salivary proline-rich protein P-B [Homo sapiens]	4.3
772	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.022	3021699	(AB005298) BAI 2 [Homo sapiens]	0.64
773	X71932	H.sapiens XB gene for tenascin-X, intron 14	0.022	627059	liver stage antigen LSA-1 - Plasmodium falciparum >gi\|9916 (X56203) liver stage antigen	0.058
774	X87369	C.perfringens nanH gene & ORF1,2,3 & 4	0.022	2062407	(U78975) poly(ADP-ribose) glycohydrolase [Bos taurus]	0.056

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					U1 SMALL NUCLEAR	
775	Y14971	Gallus gallus mRNA for K60 protein	0.022	134091	RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) >gi\|85864\|pir\|\|S02016 U1 snRNP 70K protein - African clawed frog >gi\|65179 (X12430) U1 70K [Xenopus laevis]	0.032
776	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi\|1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
777	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi\|1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
778	U57645	Human helix-loop-helix proteins Id-1 (ID-1) and Id-1' (ID-1) genes, complete cds	0.021	<NONE>	<NONE>	<NONE>
779	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	<NONE>	<NONE>	<NONE>
780	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
781	L04787	Borrelia hermsii outer membrane lipoprotein	0.021	<NONE>	<NONE>	<NONE>
782	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
783	L36890	Saccharomyces cerevisiae mitochondrion transfer RNA-Thr1 (tRNA-Thr) gene; transfer RNA-Val (tRNA-Val) gene; oxi2 gene, complete cds; ORF2 and origin of replication (ori5).	0.021	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
784	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.021	<NONE>	<NONE>	<NONE>
785	M87504	Tetrahymena thermophila histone H3 (HHT2) gene, complete cds	0.021	<NONE>	<NONE>	<NONE>
786	U94346	Human calpain-like protease (htra-3) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
787	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
788	U36530	Pongo pygmaeus CT microsatellite, clone #1, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus)	0.021	<NONE>	<NONE>	<NONE>
789	X03833	Human gene for interleukin 1 alpha (IL-1 alpha)	0.021	416974	EARLY TRANSCRIPTION FACTOR 70 KD SUBUNIT	8.9
790	U20806	Dictyostelium discoideum guanine nucleotide-binding protein alpha subunit 5 (G alpha 5) gene, complete cds.	0.021	1401211	(U58510) RNA helicase homolog [Chlorarachnion CCMP621]	8.8
791	Z59258	H.sapiens CpG DNA, clone 13d2, reverse read cpg13d2.rt1c .	0.021	3121732	ACONITATE HYDRATASE (CITRATE HYDRO-LYASE) (ACONITASE) >gi\|2183256 (AF002133) aconitase [Mycobacterium avium]	7.0
792	AF030692	Plasmodium falciparum strain 7G8 chloroquine resistance candidate protein (cg2) gene, complete cds	0.021	3024190	NINE PROTEIN >gi\|2120251\|pir\|\|S66581 hypothetical protein 56 - phage 82 >gi\|1051114 (X92588) orf56; related to nin60 (ninE) of bacteriophage lambda	5.8
793	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	2341037	(AC000104) F19P19.17 [Arabidopsis thaliana]	4.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					NUCLEAR FACTOR NF-	
794	D86566	Human DNA for NOTCH4, partial cds	0.021	1708619	KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT]	3.1
795	L11648	Streptomyces coelicolor sigma factor (rpoX) gene, complete cds.	0.021	79833	hypothetical 119.5K protein (uvrA region) - Micrococcus luteus	1.8
796	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	128000	NEUROENDOCRINE CONVERTASE 1 PRECURSOR (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) propeptide processing protease [Mus cookii]	1.0
797	U30938	Rattus norvegicus microtubule-associated protein 2	0.021	468600	(X74416) beta-3 integrin [Takifugu rubripes]	1.0
798	D82364	Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52	0.021	693723	27 kda amelogenin {alternatively spliced}	0.61
799	U40041	Gallus gallus eHAND mRNA, complete cds	0.021	3449308	(AB011541) MEGF8 [Homo sapiens]	0.21
800	X71932	H.sapiens XB gene for tenascin-X, intron 14	0.021	627059	liver stage antigen LSA-1 - Plasmodium falciparum >gi\|9916 (X56203) liver stage antigen	0.054
801	AF042333	Oryza sativa 24-methylene lophenol C24(1)methyltransferase mRNA, complete cds	0.021	854065	(X83413) U88 [Human herpesvirus 6]	0.014
802	L37380	Rat apical endosomal glycoprotein mRNA, complete cds.	0.021	3334377	TRANSMEMBRANE PROTEASE, SERINE 2	1e-05
803	AF003133	Caenorhabditis elegans cosmid T21E3	0.021	1709997	DNA REPAIR PROTEIN RAD18 >gi\|1150622 protein rad18 [Schizosaccharomyces pombe]	3e-08

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
804	X57689	Rabbit mRNA for calcium channel BI-2 (lambda CBP109 and CB101)	0.021	2959370	(AL022117) hypothetical protein	1e-10
805	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.021	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	5e-11
806	X77753	H.sapiens TROP-2 gene	0.021	1723657	HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi\|2132587\|pir\|\|S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi\|1323010\|gnl\|PID\|e243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	5e-11
807	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.021	2137872	zinc finger protein PZF - mouse >gi\|453376	2e-19
808	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
809	AJ224935	Homo sapiens Promotor Region and PCK2 gene	0.020	<NONE>	<NONE>	<NONE>
810	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
811	X99941	A.thaliana GBF1 gene	0.020	<NONE>	<NONE>	<NONE>
812	X65138	M.musculus mRNA for tyrosine kinase > :: gb\|S57168\|S57168 Sek=Eph-related receptor protein tyrosine kinase [mice, mRNA, 4242 nt]	0.020	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
813	L04787	Borrelia hermsii outer membrane lipoprotein	0.020	<NONE>	<NONE>	<NONE>
814	AJ223633	Enterococcus faecium genes encoding enterocin L50A and enterocin L50B plus 5' and 3' flanking regions	0.020	<NONE>	<NONE>	<NONE>
815	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AE001539	Helicobacter pylori, strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [Saccharomyces cerevisiae]	8.4
817	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	94173	pol polyprotein - Chinese hamster intracisternal A-particle CHIAP34	8.0
818	M55264	Herpesvirus saimiri dihydrofolate reductase (DHFR) and snRNA (HSUR) genes, complete cds.	0.020	2924250	(Z98745) dJ29K1.2 [Homo sapiens]	6.5
819	AF052163	Homo sapiens clone 24456 mRNA sequence	0.020	1706288	D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR) >gi\|2119482\|pir\|\|I49246 D4 dopamine receptor - mouse >gi\|758427 (U19880) D4 dopamine receptor [Mus musculus] >gi\|1095539\|prf\|\|2109259A dopamine D4 receptor [Mus musculus]	4.9
820	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	4.7
821	AF052163	Homo sapiens clone 24456 mRNA sequence	0.020	3874733	(Z67754) cDNA EST EMBL:T02354 comes from this gene; cDNA EST EMBL:D32698 comes from this gene; cDNA EST EMBL:D35411 comes from this gene	4.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
822	L11002	Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.020	552132	(K01664) Bkm-like protein [Drosophila melanogaster]	3.8
823	AE001539	Helicobacter pylori, strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [Saccharomyces cerevisiae]	3.8
824	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.020	3879798	(Z81126) similar to TPR Domain (2 domains); cDNA EST yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37... >gi\|3880220\|gnl\|PID\|e1349842 yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37...	1.3
825	U97519	Homo sapiens podocalyxin-like protein mRNA, complete cds	0.020	1345633	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE C1-tetrahydrofolate synthase [Rattus norvegicus]	0.066
826	AF003133	Caenorhabditis elegans cosmid T21E3	0.020	1709997	DNA REPAIR PROTEIN RAD18 >gi\|1150622 protein rad18 [Schizosaccharomyces pombe]	2e-07
827	U32857	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence	0.019	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					NEUROGENIC LOCUS	
828	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.019	2506381	NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) mammary gene mRNA, complete cds.], gene product [Mus musculus]	3.3
829	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.019	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T008...	6e-15
830	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.018	<NONE>	<NONE>	<NONE>
831	U24578	Human RP1 and complement C4B precursor (C4B) genes, partial cds.	0.013	478673	proline-rich protein precursor - kidney bean vulgaris]	3.1
832	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.011	<NONE>	<NONE>	<NONE>
833	U57649	Dibenzofuran-degrading bacterium DPO360 2,3-dihydroxybiphenyl 1,2-dioxygenase (bphC) gene, complete cds and 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hydrolase	0.011	<NONE>	<NONE>	<NONE>
834	X15642	Z.mays gene for phosphoenolpyruvate carboxylase	0.011	<NONE>	<NONE>	<NONE>
835	X51623	C.elegans collagen gene col-13	0.010	1695686	(D83706) pyruvate carboxylase [Bacillus stearothermophilus]	3.1
836	U83656	Rattus norvegicus NF-KB gene, promotor region	0.008	4240195	(AB020660) KIAA0853 protein [Homo sapiens]	10.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					POL POLYPROTEIN	
837	AJ222657	Homo sapiens gene encoding retina-specific guanylyl cyclase	0.008	417704	(ORF1A/1B) [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; HELICASE; PROTEASE]	7.4
838	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.008	544024	CHLORIDE CHANNEL PROTEIN, SKELETAL MUSCLE (CHLORIDE CHANNEL PROTEIN 1) (CLC-1) human >gi\|397143 (Z25587) human ClC-1 muscle chloride channel [Homo sapiens] >gi\|398161 (Z25884) human ClC-1 muscle chloride channel [Homo sapiens]	4.6
839	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	532468	(U13643) similar to reverse transcriptase; possible pseudogene [Caenorhabditis elegans]	3.8
840	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	4101160	(AF002589) cytochrome oxidase I [Austrofundulus limnaeus]	2.7
841	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.008	1711520	SRB-8/9 PROTEIN >gi\|1334996	1.6
842	U48734	Human non-muscle alpha-actinin mRNA, complete cds	0.008	2829922	(AC002291) extensin [Arabidopsis thaliana]	0.11
843	U66669	Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D16492	Mouse mRNA for P100 serine protease of Ra-reactive factor (RaRF), complete cds	0.007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human				
845	D90923	immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds, isolate 03S	0.007	<NONE>	<NONE>	<NONE>
846	AB011087	Homo sapiens mRNA for KIAA0515 protein, partial cds	0.007	<NONE>	<NONE>	<NONE>
847	AE000688	Aquifex aeolicus section 20 of 109 of the complete genome	0.007	<NONE>	<NONE>	<NONE>
848	X63723	B.bovis WC1.1 mRNA	0.007	<NONE>	<NONE>	<NONE>
849	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
850	J00097	Human beta globin region Alu repetitive sequence type T.	0.007	<NONE>	<NONE>	<NONE>
851	D90923	Human immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds, isolate 03S	0.007	<NONE>	<NONE>	<NONE>
852	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	X91618	T.castaneum hunchback gene	0.007	<NONE>	<NONE>	<NONE>
854	X03838	Rat nontranscribed spacer (NTS) downstream of 28S rRNA gene	0.007	<NONE>	<NONE>	<NONE>
855	M55049	Rattus norwegicus interleukin-2 receptor alpha chain (CD25) mRNA, complete cds.	0.007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
856	Z64318	H.sapiens CpG DNA, clone 9e2, reverse read cpg9e2.rt1a .	0.007	<NONE>	<NONE>	<NONE>
857	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
858	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
859	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
860	X95276	P.falciparum complete gene map of plastid-like DNA	0.007	<NONE>	<NONE>	<NONE>
861	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
862	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
863	AB000383	Leucania seperata nuclear polyhedrosis virus DNA for p13, xe, envelope protein, complete cds	0.007	<NONE>	<NONE>	<NONE>
864	D86566	Human DNA for NOTCH4, partial cds	0.007	<NONE>	<NONE>	<NONE>
865	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
866	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	3047072	(AF058825) No definition line found [Arabidopsis thaliana]	8.9
867	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	975754	(U29359) SpaO [Salmonella enterica]	8.6
868	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4
869	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	2499568	PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL/D-ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] >gi\|1171337 melanogaster]	8.3
870	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	4092077	(AF095353) toll-like receptor 4 mutant [Mus musculus]	6.2
871	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	151377	(M80653) tetraheme [Pseudomonas stutzeri]	6.2
872	L42319	Bos taurus (clone Sal3.8) tristetraprolin	0.007	2507337	TRANSCRIPTION TERMINATION FACTOR RHO	5.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
873	M59815	Human complement component C4A gene, exons 10 through 41.	0.007	3876769	(Z69637) Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HUMAN); cDNA EST yk219g12.5 comes from this gene; cDNA EST yk319d8.5 comes from this gene; cDNA EST yk339d11.5 comes from this gene; cDNA EST yk371c9.3...	5.3
874	X63723	B.bovis WC1.1 mRNA	0.007	2969893	(AJ001858) human SIM2 [Homo sapiens]	5.3
875	AB009864	Expression vector pME18S-FL3, complete sequence	0.007	2137618	p45 NF-E2 related factor 2 - mouse musculus]	5.1
876	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	2804497	(AF043705) contains similarity to C2H2-type zinc fingers	5.0
877	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.007	440298	(L27469) product of alternative splicing [Drosophila melanogaster]	4.7
878	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	1185062	(L75945) flagellar export protein [Borrelia burgdorferi]	4.1
879	AF027735	Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds	0.007	2394390	(AF017434) pmi-like gene product [Methylobacterium extorquens]	4.0
880	AF105228	Bos taurus tuftelin mRNA, complete cds	0.007	3036802	(AL022373) putative protein	3.9
881	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	2500814	HYPOTHETICAL 60.2 KD PROTEIN T27F2.1 IN CHROMOSOME V >gi\|3880311\|gnl\|PID\|e1349855 BX42 (SW:BX42_DROME); cDNA EST EMBL:C07233 comes from this gene; cDNA EST EMBL:C08532 comes from this gene; cDNA EST yk501h10.3 comes from this gene; cDNA EST yk501f1.3...	3.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U78289) tylactone synthase	
882	X93567	L.major mRNA for beta-tubulin (1404bp)	0.007	2317862	modules 4 & 5 [Streptomyces fradiae]	3.0
883	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	3881103	(AL032646) predicted using Genefinder; cDNA EST EMBL:D76407 comes from this gene; cDNA EST EMBL:C08999 comes from this gene; cDNA EST yk199b12.5 comes from this gene; cDNA EST yk282a4.5 comes from this gene; cDNA EST EMBL:C0...	2.7
884	AF041056	Homo sapiens WSCR4 gene, exons 3 and 4	0.007	135817	THROMBIN RECEPTOR PRECURSOR human >gi\|339677 (M62424) thrombin receptor [Homo sapiens]	2.2
885	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	1723518	HYPOTHETICAL 32.2 KD PROTEIN C22E12.04 IN CHROMOSOME I >gi\|1220279 (Z70043) unknown	2.1
886	M74798	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene, 3' end.	0.007	1001282	(D64003) polyA polymerase	1.9
887	Z62997	H.sapiens CpG DNA, clone 76g11, reverse read cpg76g11.rt1a .	0.007	1176532	HYPOTHETICAL 111.9 KD PROTEIN C34E10.8 IN CHROMOSOME III >gi\|500731 (U10402) weakly similar to protein C kinase substrate [Caenorhabditis	1.8
888	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	2498317	DVA-1 POLYPROTEIN PRECURSOR nematode polyprotein antigen precursor [Dictyocaulus viviparus] >gi\|1585421\|prf\|\|2124414A polyprotein antigen/allergen [Dictyocaulus viviparus]	1.2
889	L29426	Synechocystis species (strain PCC 6803) drgA gene, complete cds.	0.007	3882275	(AB018320) KIAA0777 protein [Homo sapiens]	1.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
890	D83329	Mus musculus DNA for prostaglandin D2 synthase, complete cds	0.007	1001741	(D64004) hypothetical protein	0.97
891	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	1723928	HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR YGL149w - yeast (Saccharomyces	0.94
892	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	121452	GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR >gi\|82606\|pir\|\|A24266 glutenin high molecular weight chain 12 precursor - wheat >gi\|21779	0.79
893	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	927287	(U30294) ORF2 [Prevotella ruminicola]	0.35
894	Y11918	H.sapiens IMAGE cDNA clone 26881	0.007	1055188	(U40061) contains similarity to transmembrane domains like those found in sugar transporter proteins	0.26
895	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.21
896	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.20
897	Z65719	H.sapiens CpG DNA, clone 54c10, reverse read cpg54c10.rt1a .	0.007	1097307	HIC-1 gene [Homo sapiens]	0.20
898	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.007	1174915	UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) >gi\|284488\|pir\|\|S28381 utrophin protein) [Homo sapiens]	0.002
899	AF051730	Mus musculus cathepsin S (CatS) gene, exon 6	0.007	1707017	(U78721) RNA helicase isolog [Arabidopsis thaliana]	0.001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Oryctolagus				
900	U62398	cuniculus gp42/basigin/OX-47/HT7 mRNA, complete cds.	0.007	2370494	(Z98944) hypothetical protein	2e-04
901	X76341	M.musculus glutathione reductase mRNA.	0.007	3513303	(AC005594) R26984_1 [Homo sapiens]	8e-07
902	M26215	Rat (lambda 20B0.5) M-type 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase	0.007	3036809	(AL022373) putative protein	6e-15
903	AB007902	Homo sapiens KIAA0442 mRNA, partial cds	0.007	2662165	(AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]	2e-17
904	U93364	Lactococcus lactis cremoris plasmid pNZ4000 insertion sequence IS982 putative transposase gene and eps gene cluster (epsRXABCDEFGHIJKL), complete cds	0.007	2731377	(U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]	1e-31
905	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
906	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
907	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
908	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
909	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
910	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
911	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
912	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
913	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
914	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
915	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
916	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	4049856	(AF063866) ORF MSV064 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	9.6
917	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	3880536	(Z82070) predicted using Genefinder; similar to Lectin C-type domain short and long forms (2 domains); cDNA EST EMBL:C10633 comes from this gene; cDNA EST EMBL:C12424 comes from this gene; cDNA EST yk191e7.3 comes from this ...	7.9
918	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	3877761	(Z81552) F56G4.1 [Caenorhabditis elegans] >gi\|3878615\|gnl\|PID\|e1348240 (Z83118) F56G4.1	7.5
919	X80289	H.sapiens PTPL1 mRNA for protein tyrosine phosphatase	0.006	1168791	CATHEPSIN E PRECURSOR precursor - rabbit >gi\|402729 (L08418) procathepsin E	7.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DIACYLGLYCEROL	
920	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	1346371	KINASE, BETA DIACYLGLYCEROL KINASE) >gi\|477059\|pir\|\|A47744 diacylglycerol kinase (EC 2.7.1.107) beta - rat 90kDa-diacylglycerol kinase [Rattus	5.5
921	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.006	2196567	(D88588) lipoprotein [Escherichia coli]	4.3
922	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	4.3
923	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	1388166	(U58282) Bowel [Drosophila melanogaster]	4.3
924	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	2496785	HYPOTHETICAL 20.1 KD PROTEIN Y4YS	4.2
925	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi\|101170\|pir\|\|A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.7
926	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi\|101170\|pir\|\|A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.5
927	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	3258584	(U41263) The 3' UTR of this gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.0
928	U33949	Human Down Syndrome region of chromosome 21, genomic sequence, clone A12H1-1A6.	0.006	3850997	(AF067150) beta-hydroxyacyl-ACP dehydratase precursor	1.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
929	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	3881220	(AL032630) predicted using Genefinder	1.2
930	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	1346439	P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P)	0.90
931	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	2736338	(AF038623) contains similarity to RNA recognition motifs	0.84
932	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	121452	GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR >gi\|82606\|pir\|\|A24266 glutenin high molecular weight chain 12 precursor - wheat >gi\|21779	0.51
933	M25140	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4.	0.006	3257709	(AP000005) 115aa long hypothetical protein [Pyrococcus horikoshii]	0.49
934	Z46906	Sus scrofa.	0.006	1144571	(U35363) latent TGF-beta binding protein-2 [Bos taurus]	0.076
935	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	1515302	(X97720) retrovirus restriction polypeptide [Mus musculus]	4e-05
936	M23236	Mouse proline-rich protein (M14) gene, complete cds, clones MC(14, 16,22).	0.006	3372354	(AF041104) atrophin-1 like protein [Homo sapiens]	3e-05
937	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.004	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
938	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.004	<NONE>	<NONE>	<NONE>
939	M30447	Human lymphocyte receptor (Fc-epsilon-RII-alpha) gene, promoter and 5' flank.	0.004	2832355	(Y14074) HMG protein [Arabidopsis thaliana]	7.8
940	M33940	Human Val-tRNA and Lys-tRNA genes.	0.004	122917	HEMAGGLUTININ PRECURSOR	7.7
941	D90809	E.coli genomic DNA. Kohara clone #318(37.2-37.6 min.)	0.004	3880435	(Z66521) similar to n-acetyllactosamine synthase; cDNA EST yk258c9.5 comes from this gene	1.7
942	X54500	H.sapiens gene for factor IX (F9IN1A4)	0.003	1492074	(U60315) MC131L [Molluscum contagiosum virus subtype 1]	2.9
943	M17196	A.californica (marine gastropod mollusc) neuropeptide gene (ganglion R14), exon 1, 5' end.	0.003	91868	U1 snRNP 70K protein (long form) - mouse protein [Mus musculus]	2.0
944	M13498	Mouse renal kallikrein gene mGK-6, exon 1.	0.003	3979818	(Z49967) cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA EST EMBL:D65790 comes from this gene; cDNA EST EMBL:D70463 comes from this gene; cDNA EST EMBL:D66620 comes from this gene; ...	4e-14
945	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
946	M66390	Human GP91-PHOX gene promoter region.	0.002	<NONE>	<NONE>	<NONE>
947	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
948	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
949	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
950	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
951	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
952	AF003512	Chelonus sp. 16S ribosomal RNA gene. partial sequence > :: gb\|AF029115\|AF029115 Chelonus sp. 16S ribosomal RNA gene. mitochondrial gene for mitochondrial RNA, partial sequence	0.002	<NONE>	<NONE>	<NONE>
953	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
954	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
955	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
956	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
957	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
958	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
959	AB014560	Homo sapiens mRNA for KIAA0660 protein, complete cds	0.002	<NONE>	<NONE>	<NONE>
960	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
961	U72790	Homo sapiens cosmic clone U90A4 from Xp22.1-22.2, complete sequence [Homo sapiens]	0.002	<NONE>	<NONE>	<NONE>
962	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
963	Z79119	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA22H6	0.002	<NONE>	<NONE>	<NONE>
964	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
965	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
966	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
967	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
968	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
969	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
970	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
971	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
972	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
973	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
974	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
975	U29874	Human Flt3 ligand gene and Flt3 ligand alternatively spliced isoform gene, complete cds.	0.002	<NONE>	<NONE>	<NONE>
976	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
977	AF104631	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
978	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		S.tuberosum mRNA				
979	X98890	for inorganic phosphate transporter, StPT1	0.002	<NONE>	<NONE>	<NONE>
980	Y13298	Homo sapiens GDP dissociation inhibitor beta pseudogene	0.002	<NONE>	<NONE>	<NONE>
981	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
982	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
983	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	3873694	(Z67734) cDNA EST EMBL:T01290 comes from this gene; cDNA EST EMBL:T01291 comes from this gene [Caenorhabditis elegans]	9.6
984	X53419	M.mulatta gamma-globin-1(G), gamma-globin-2(A) genes and L1 LINE element	0.002	576741	(U15669) cytochrome b [Myrmecia banksi]	8.1
985	AB012043	Homo sapiens mRNA for NBR13, complete cds	0.002	2828297	(AL021687) putative protein	8.1
986	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	3873694	(Z67734) cDNA EST EMBL:T01290 comes from this gene; cDNA EST EMBL:T01291 comes from this gene [Caenorhabditis elegans]	8.1
987	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	3152567	(AC002986) Contains similarity to membrane associated salt-inducible protein gb\|AF007269 from A. thaliana.	7.6
988	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	2244848	(Z97337) imidazoleglycerol-phosphate dehydratase [Arabidopsis thaliana]	6.6
989	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	251893	(S40543) low density lipoprotein receptor, LDL receptor [human, Peptide Partial Mutant, 59 aa] [Homo sapiens]	6.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
990	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.002	3599339	(AF081111) ORF2 [Mus musculus domesticus]	5.8
991	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	2920539	(AF016408) integral outer membrane protein P66 [Borrelia hermsii]	5.7
992	X97009	M.domestica mRNA for yolk protein-2	0.002	3641302	(AF087454) potassium channel [Rattus norvegicus]	5.3
993	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	133100	60S RIBOSOMAL PROTEIN L40 (CEP52)	5.2
994	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	3218463	(AJ006350) surface [Duck hepatitis B virus]	5.2
995	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	540270	(U14635) weak similarity to NADH dehydrogenase	5.1
996	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	2133677	I71-7 protein - fruit fly (Drosophila melanogaster) >gi\|775239 (U24246) I71-7 [Drosophila melanogaster] >gi\|940000 (U23836) I71-7 gene product L71-7 gene [Drosophila melanogaster]	4.9
997	AB014560	Homo sapiens mRNA for KIAA0660 protein, complete cds	0.002	2414291	(Z99265) T05F1B.3 [Caenorhabditis elegans]	4.9
998	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	1723093	HYPOTHETICAL 43.3 KD PROTEIN CY50.24 >gi\|1480328\|gnl\|PID\|e254886 (Z77137) hypothetical protein Rv1258c [Mycobacterium tuberculosis]	4.6
999	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	3024136	PUTATIVE CELL DIVISION TOPOLOGICAL SPECIFICITY FACTOR >gi\|2224465\|gnl\|PID\|d1021527	4.4
1000	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	1360834	transcriptional control protein 50 - equine herpesvirus 2 >gi\|695223 (U20824) ORF 50 [Equine herpesvirus 2]	3.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Brassica rapa mRNA				
1001	AB012106	for SRK45, complete cds	0.002	2290408	(U92042) mating type 1 pheromone precursor	3.7
1002	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	1362802	gastric mucin - human (fragment) >gi\|547517	2.9
1003	U88583	Plasmodium falciparum acyl-CoA ligase antigen gene, complete cds	0.002	3766236	(AF095287) pituitary tumor transforming gene protein 1 hPTTG [Homo sapiens]	2.9
1004	Z54983	H.sapiens CpG DNA, clone 181g2, forward read cpg181g2.ft1a .	0.002	139633	T4 PROTEIN >gi\|419180\|pir\|\|F43692 T4 protein - rabbit fibroma virus	2.8
1005	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.002	4205068	(U69592) nef protein [Human immunodeficiency virus type 1]	2.8
1006	U42430	Mesocricetus auratus CD36 mRNA, complete cds	0.002	1480370	(X99406) protein kinase [Xenopus laevis]	2.8
1007	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	125356	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (C-FES) >gi\|2117868\|pir\|\|I48347 protein-tyrosine kinase-related protein - mouse	2.2
1008	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.002	951451	(L46818) TCJ3 [Trypanosoma cruzi]	1.9
1009	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	1078029	hypothetical protein YOR022c - yeast OR26.12 [Saccharomyces cerevisiae]	1.8
1010	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	1360893	klcB protein - plasmid RK2 >gi\|603901	1.2
1011	U92894	Homo sapiens LERK-6 (EPLG6) gene, exons 2 and 3	0.002	113670	!!!! ALU CLASS E WARNING ENTRY !!!!	1.2
1012	Z54983	H.sapiens CpG DNA, clone 181g2, forward read cpg181g2.ft1a .	0.002	3688090	(AC005757) R32611_2 [Homo sapiens]	1.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z66521) similar to n-	
1013	D90809	E.coli genomic DNA, Kohara clone #318(37.2-37.6 min.)	0.002	3880435	acetyllactosamine synthase; cDNA EST yk258c9.5 comes from this gene	0.82
1014	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	1360834	transcriptional control protein 50 - equine herpesvirus 2 >gi\|695223 (U20824) ORF 50 [Equine herpesvirus 2]	0.67
1015	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.002	3876367	(Z69360) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans] Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]	0.66
1016	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	417782	SMP2 PROTEIN >gi\|320853\|pir\|\|S30911 SMP2 protein - yeast (Saccharomyces cerevisiae) gene [Saccharomyces cerevisiae]	0.53
1017	AF104631	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds	0.002	190247	(J04564) snRNP polypeptide B [Homo sapiens]	0.34
1018	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	1334398	(X15081) MURF2 protein (AA 1-348)	0.30
1019	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	1334398	(X15081) MURF2 protein (AA 1-348)	0.29
1020	U91524	Drosophila melanogaster ferritin subunit 1	0.002	3257342	(AP000004) 879aa long hypothetical purine NTPase [Pyrococcus horikoshii]	0.26

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1021	AJ225089	Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform	0.002	3513512	(AF043944) nongradient byssal precursor [Mytilus edulis]	0.17
1022	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	548937	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR	0.14
1023	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	2707911	(AF038383) capsid protein [Feline calicivirus]	0.13
1024	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	2498506	PROLINE-RICH PROTEIN LAS17 yeast (Saccharomyces cerevisiae) protein [Saccharomyces cerevisiae]	0.085
1025	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	3402186	Chain A, Structure Of Tobacco Ringspot Virus	0.048
1026	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	387111	(J03723) carbohydrate binding protein 35 [Mus musculus]	0.002
1027	AF104631	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds	0.002	35871	(X64002) RAP74 [Homo sapiens] >gi\|228483\|prf\|\|1804353A transcription factor RAP74 [Homo sapiens]	6e-09
1028	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.002	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T008...	3e-14

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z49967) cDNA EST	
1029	M13498	Mouse renal kallikrein gene mGK-6, exon 1.	0.002	3979818	EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA EST EMBL:D65790 comes from this gene; cDNA EST EMBL:D70463 comes from this gene; cDNA EST EMBL:D66620 comes from this gene: ...	3e-14
1030	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	3879755	(Z80220) similar to nucleotide binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST EMBL:M89054 comes from this gene; cDNA EST EMBL:D26713 comes from this gene; cDNA EST EMBL:D26718 comes from this gene; cDNA...	1e-15
1031	J03526	Yeast (S.cerevisiae) aspartokinase gene, complete cds.	0.002	3980554	(AC004849) similar to several hypothetical proteins: U70849 (PID:g1572765), U00043 (PID:g470341), Z50070	3e-17
1032	U23412	Caenorhabditis elegans cosmid T10F2.	0.002	727448	(U23412) similar to proteins in the mitochondrial carrier family [Caenorhabditis elegans]	3e-18
1033	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.002	2315828	(AF016687) similar to alpha-actinin [Caenorhabditis elegans]	7e-26
1034	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.001	<NONE>	<NONE>	<NONE>
1035	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.001	<NONE>	<NONE>	<NONE>
1036	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.001	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1037	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.001	<NONE>	<NONE>	<NONE>
1038	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.001	2338550	(AF013284) keratin [Sparus aurata]	0.33
1039	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	9e-04	<NONE>	<NONE>	<NONE>
1040	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	9e-04	<NONE>	<NONE>	<NONE>
1041	Y00493	Aspergillus nidulans DNA for transformation enhancing fragment ans1	9e-04	<NONE>	<NONE>	<NONE>
1042	AB012106	Brassica rapa mRNA for SRK45, complete cds	9e-04	<NONE>	<NONE>	<NONE>
1043	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	9e-04	<NONE>	<NONE>	<NONE>
1044	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-04	3880252	(Z82055) similar to Zinc finger, C4 type (two domains) [Caenorhabditis elegans]	7.8
1045	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	9e-04	3522957	(AC004411) unknown protein [Arabidopsis thaliana]	3.7
1046	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-04	1945621	(D84435) HMW prekininogen [Mus sp.]	3.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1047	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	9e-04	2633169	(Z99108) similar to iron(III) dicitrate transport permease [Bacillus subtilis] subtilis]	0.56
1048	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	9e-04	3876299	(Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorha... >gi\|3880760\|gnl\|PID\|e1350302 (AL021474) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenor...	3e-15
1049	AB012105	Brassica rapa mRNA for SLG45, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1050	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	8e-04	<NONE>	<NONE>	<NONE>
1051	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1052	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1053	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1054	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1055	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1056	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1057	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1058	Y00493	Aspergillus nidulans DNA for transformation enhancing fragment ans1	8e-04	<NONE>	<NONE>	<NONE>
1059	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1060	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1061	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1062	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1063	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-04	<NONE>	<NONE>	<NONE>
1064	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-04	<NONE>	<NONE>	<NONE>
1065	X55064	Chinese hamster metallothionein I gene	8e-04	4218005	(AC006135) putative vicilin storage protein	9.4
1066	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-04	2072326	(U95843) DNA polymerase [Murine adenovirus type 1]	9.3
1067	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-04	126709	MALTOSE OPERON PERIPLASMIC PROTEIN PRECURSOR >gi\|478599\|pir\|\|S20600 malM protein - Salmonella typhimurium >gi\|47770 (X54292) malM	9.1
1068	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	3914984	FERRICHROME SIDEROPHORE PEPTIDE SYNTHETASE >gi\|2731633 (U62738) ferrichrome siderophore peptide synthetase [Ustilago maydis]	7.2
1069	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	8e-04	1176647	SRA-2 PROTEIN chemosensory receptor [Caenorhabditis elegans]	6.7
1070	D63861	Human DNA for cyclophilin 40, complete cds	8e-04	1177049	ZINC FINGER PROTEIN ZMS1 YJR127c [Saccharomyces cerevisiae]	6.6
1071	U09817	Human adenine phosphoribosyltransferase (APRT) gene, 5' region and partial cds	8e-04	3413862	(AB007919) KIAA0450 protein [Homo sapiens]	6.5
1072	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	8e-04	1788209	(AE000283) high-affinity L-arabinose transport system; membrane protein, fragment 1 [Escherichia coli]	5.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PHOSPHOENOLPYRUVATE	
1073	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1168759	CARBOXYLASE phosphoenolpyruvate carboxylase (ppc) homolog - Haemophilus influenzae (strain Rd KW20) >gi\|1574482	5.0
1074	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	2496785	HYPOTHETICAL 20.1 KD PROTEIN Y4YS	4.9
1075	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	2622654	(AE000913) heavy-metal transporting CPx-type ATPase	3.8
1076	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	992917	(L42814) acetyl CoA carboxylase [Glycine max]	3.2
1077	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	8e-04	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi\|101170\|pir\|\|A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	3.0
1078	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	1020191	(U31781) putative [Human papillomavirus type 23]	3.0
1079	L42319	Bos taurus (clone Sal3.8) tristetraprolin	8e-04	2914119	(U42839) F11C7.5 [Caenorhabditis elegans]	2.5
1080	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	8e-04	1336008	(U56104) acyl-ACP thioesterase [Cuphea wrightii]	2.2
1081	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-04	3122972	PROBABLE TRNA	2.2
1082	AJ223734	Sus scrofa SCAMP1 gene, exon 1 and joined CDS	8e-04	2117181	(Z95584) mcr [Mycobacterium tuberculosis]	1.4
1083	AJ223734	Sus scrofa SCAMP1 gene, exon 1 and joined CDS	8e-04	2117181	(Z95584) mcr [Mycobacterium tuberculosis]	1.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1084	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	3560124	(AJ007670) LGMD2B protein [Homo sapiens]	1.1
1085	U19261	Human Epstein-Barr virus-induced protein mRNA, complete cds.	8e-04	1730009	NUCLEOPROTEIN TPR >gi\|633226	0.62
1086	U19261	Human Epstein-Barr virus-induced protein mRNA, complete cds.	8e-04	1730009	NUCLEOPROTEIN TPR >gi\|633226	0.57
1087	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-04	137748	PROBABLE E5 PROTEIN	0.34
1088	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	1709513	PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, GAMMA ISOFORM (PI3-KINASE P110 SUBUNIT GAMMA) (PTDINS-3-KINASE P110) (PI3K)	0.039
1089	Z83321	A.thaliana 16 kb chromosome 1 DNA fragment	8e-04	1353139	PROBABLE PSEUDOURIDYLATE SYNTHASE E02H1.3 (PSEUDOURIDINE SYNTHASE) DEG-1 protein (Swiss Prot accession number P31115); cDNA EST EMBL:D70252 comes from this gene; cDNA EST EMBL:D66512 comes from this gene; cDNA EST yk366h4.3 comes from this gene; cDNA EST yk366h4.5 ...	1e-12
1090	AF035299	Homo sapiens clone 23863 mRNA, partial cds	8e-04	3252824	(AC004382) Unknown gene product [Homo sapiens]	2e-70
1091	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1092	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1093	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1094	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1095	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1096	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1097	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1098	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	<NONE>	<NONE>	<NONE>
1099	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1100	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1101	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1102	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1103	AB012106	Brassica rapa mRNA for SRK45, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1104	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1105	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1106	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1107	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1108	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1109	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1110	AF016434	Caenorhabditis elegans cosmid F58D7	7e-04	<NONE>	<NONE>	<NONE>
1111	U52427	Human RNA polymerase II seventh subunit (rpb-7) gene, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1112	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1113	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1114	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
1115	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	3876415	(Z81070) similar to fasciclin; cDNA EST EMBL:D67949 comes from this gene; cDNA EST EMBL:D64648 comes from this gene; cDNA EST EMBL:D64797 comes from this gene; cDNA EST EMBL:C11873 comes from this gene; cDNA EST EMBL:C10283 ...	9.9
1116	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	1076558	hypothetical protein x (nad5 exon c 5' region) - evening primrose mitochondrion	7.8
1117	AB012106	Brassica rapa mRNA for SRK45, complete cds	7e-04	3875964	(Z78015) Similarity to Drosophila Cadherin-related tumor suppressor precursor gene; cDNA EST EMBL:T00146 comes from this gene; cDNA EST EMBL:D33921 comes from this gene; c... Drosophila Cadherin-related tumor suppressor precursor gene; cDNA EST EMBL:T00146 comes from this gene; cDNA EST EMBL:D33921 comes from this gene; c...	7.7
1118	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	669033	(U20864) similar to mucin; similar to lactoperoxidase, thyroid peroxidase, myeloperoxidase, and eosinophil peroxidase [Caenorhabditis elegans]	6.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1119	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	3880252	(Z82055) similar to Zinc finger, C4 type (two domains) [Caenorhabditis elegans]	6.2
1120	AB012106	Brassica rapa mRNA for SRK45, complete cds	7e-04	123052	FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi\|87410\|pir\|\|A36403 ferrochelatase (EC 4.99.1.1) precursor - human precursor [Homo sapiens]	6.1
1121	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	130319	PLASMINOGEN >gi\|2144494\|pir\|\|PLPG plasmin (EC 3.4.21.7) precursor - pig (fragment)	6.0
1122	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	212713	(J03579) c-tkl tyrosine kinase (EC 2.7.1.112) [Gallus gallus]	5.9
1123	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	118053	APOCYTOCHROME F PRECURSOR chloroplast >gi\|11845 (Z00044) cytochrome f [Nicotiana tabacum] >gi\|225213\|prf\|\|1211235AU cytochrome f	5.9
1124	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	118053	APOCYTOCHROME F PRECURSOR chloroplast >gi\|11845 (Z00044) cytochrome f [Nicotiana tabacum] >gi\|225213\|prf\|\|1211235AU cytochrome f	5.9
1125	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	7e-04	3892137	(Z69883) similar to member of worm-specific protein family; cDNA EST yk238b3.5 comes from this gene [Caenorhabditis elegans] of worm-specific protein family; cDNA EST yk238b3.5 comes from this gene [Caenorhabditis elegans]	5.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1126	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	3688181	(AL031804) putative protein (fragment)	5.7
1127	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	4176525	(AL035263) hypothetical protein	4.6
1128	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	1834495	(X98248) sortilin [Homo sapiens]	3.7
1129	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	7e-04	567166	(L03172) This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal.	3.4
1130	AB012105	Brassica rapa mRNA for SLG45, complete cds	7e-04	1142657	(U22680) X2 box repressor [Homo sapiens]	2.9
1131	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	3122972	PROBABLE TRNA	2.0
1132	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	1834495	(X98248) sortilin [Homo sapiens]	1.1
1133	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	3257709	(AP000005) 115aa long hypothetical protein [Pyrococcus horikoshii]	0.52
1134	U62021	Mus musculus neuronal pentraxin 1 (NPTX1) gene, complete cds	7e-04	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	0.022
1135	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	1174915	UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) >gi\|284488\|pir\|\|S28381 utrophin protein) [Homo sapiens]	0.013

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana				
1136	AJ005813	mRNA for neoxanthin cleavage enzyme	7e-04	1707017	(U78721) RNA helicase isolog [Arabidopsis thaliana]	0.001
1137	U95607	Mus musculus testis specific DNAj-homolog mRNA, complete cds	7e-04	3880170	(Z54216) similar to DNAJ protein; cDNA EST EMBL:T00334 comes from this gene; cDNA EST EMBL:T01898 comes from this gene; cDNA EST EMBL:T02311 comes from this gene; cDNA EST EMBL:D72569 comes from this gene; cDNA EST yk375e5.3...	2e-15
1138	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	2677676	(AC002467) DRA protein (down-regulated in adenoma); sulfate transporter; match to P40879 (PID:g729367) [Homo sapiens]	7e-60
1139	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	6e-04	<NONE>	<NONE>	<NONE>
1140	M32475	Rattus norvegicus carcinoembryonic antigen-related protein (CGM4) gene, exons 2 and 3.	4e-04	<NONE>	<NONE>	<NONE>
1141	X61444	H.sapiens TCR V-beta 6.10 gene for TCR beta chain variable region	4e-04	124091	PROBABLE PROCESSING AND TRANSPORT PROTEIN (INFECTED CELL PROTEIN 18.5) (ICP18.5 PROTEIN) protein ICP18.5 - bovine herpesvirus 2 (strain BMV)	7.4
1142	Z70295	H.sapiens GCAP-II gene	4e-04	2496201	HYPOTHETICAL PROTEIN MJECS07 Methanococcus jannaschii plasmid pURB801 >gi\|1522639	1.3
1143	M94579	Human carboxyl ester lipase (CEL) gene, complete cds.	3e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1144	M97911	Wegener's granulomatosis autoantigen proteinase 3 gene, exons 1, 2, 3, 4, and 5.	3e-04	<NONE>	<NONE>	<NONE>
1145	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1146	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1147	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1148	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1149	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1150	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	3e-04	<NONE>	<NONE>	<NONE>
1151	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1152	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1153	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1154	AF051882	carbonic anhydrase XII precursor	3e-04	<NONE>	<NONE>	<NONE>
1155	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1156	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-04	2467306	(AB000919) VHA-4 [Caenorhabditis elegans] >gi\|3879265\|gnl\|PID\|e1348752 (Z68317) similar to proteolipid protein PPA1 like protein; cDNA EST EMBL:Z14765 comes from this gene; cDNA EST EMBL:D73255 comes from this gene; cDNA EST EMBL:D72321 comes from this gene; cDNA EST EMBL:D76269 comes from this...	8.8
1157	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	3e-04	1346609	MALVOLIO PROTEIN	6.5
1158	X91890	H.sapiens regulatory region of HOXA7 gene	3e-04	1199810	(X95665) cDNA6 gene product [Brugia pahangi]	5.4
1159	AB009369	Mus musculus mRNA for G protein-coupled receptor KY411, complete cds	3e-04	3880848	(AL031633) cDNA EST yk210c11.3 comes from this gene; cDNA EST yk210c11.5 comes from this gene	5.0
1160	M94580	Human carboxyl ester lipase-like (CELL) gene.	3e-04	1628471	(Y08780) Men-8 [Silene latifolia]	4.1
1161	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	3e-04	3523135	(AF039315) transferrin binding protein A; TbpA	2.9
1162	X90761	Homo sapiens hHa2 gene	3e-04	2144023	zinc finger DNA-binding protein - rat	1.9
1163	M94579	Human carboxyl ester lipase (CEL) gene, complete cds.	3e-04	2370466	(Z98951) hypothetical protein	1.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1164	U55207	Mus musculus tissue transglutaminase gene, promoter region and partial cds	3e-04	2463203	(Y11536) SHOXa protein [Homo sapiens] homeodomain-containing protein [Homo sapiens]	0.90
1165	U55207	Mus musculus tissue transglutaminase gene, promoter region and partial cds	3e-04	2463203	(Y11536) SHOXa protein [Homo sapiens] homeodomain-containing protein [Homo sapiens]	0.80
1166	U47105	Human H105e3 mRNA, complete cds	3e-04	93127	BHV-1 protein homolog VZV9 - bovine herpesvirus 1	0.26
1167	D14479	Rat mRNA for calpain, complete cds	3e-04	477319	calpain (EC 3.4.22.17) large chain nCL-2, tissue-specific - rat >gi\|441200\|gnl\|PID\|d1003880	0.023
1168	M32514	Rat simple sequence DNA, clone 5.	3e-04	3560497	(AF023853) ElpB2 [Borrelia burgdorferi]	0.003
1169	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-04	2495704	HYPOTHETICAL PROTEIN KIAA0129 product is novel. [Homo sapiens]	4e-04
1170	X82829	B.taurus mRNA for nuclear DNA helicase II	3e-04	2880057	(AC002340) putative RNA helicase A, 5' partial	2e-19
1171	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1172	AB012105	Brassica rapa mRNA for SLG45, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1173	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1174	AB012106	Brassica rapa mRNA for SRK45, complete cds	2e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1175	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1176	Y09232	H.sapiens fertilin alpha pseudogene	2e-04	<NONE>	<NONE>	<NONE>
1177	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1178	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1179	AF072847	Homo sapiens putative swelling-activated chloride channel (CLNS1A) gene, intron 6	2e-04	<NONE>	<NONE>	<NONE>
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1181	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1182	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					EPITHELIAL DISCOIDIN	
1183	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	729008	DOMAIN RECEPTOR 1 PRECURSOR (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN-TYROSINE KINASE RTK 6) sapiens]	8.3
1184	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	2507582	HYPOTHETICAL 138.1 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION >gi\|1788436 (AE000300) putative regulator [Escherichia coli]	7.8
1185	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	2e-04	1085500	collagen alpha 1(IX) chain - mouse musculus] >gi\|744962\|prf\|\|2015346A collagen:SUBUNIT=alpha1:ISOTYPE=IX [Mus musculus]	7.8
1186	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	2623967	(Y13942) GTN Reductase [Agrobacterium radiobacter]	7.4
1187	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	2497316	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS) products receptor precursor - bovine >gi\|163651 (M91212) receptor for advanced glycosylation end products [Bos taurus]	5.3
1188	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	2e-04	1001710	(D64004) hypothetical protein	3.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana			(U41263) The 3' UTR of this	
1189	AJ005813	mRNA for neoxanthin cleavage enzyme	2e-04	3258584	gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.1
1190	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	2736338	(AF038623) contains similarity to RNA recognition motifs	0.89
1191	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	2e-04	2196567	(D88588) lipoprotein [Escherichia coli]	0.69
1192	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	3319874	(AJ006096) F-spondin [Branchiostoma floridae]	5e-04
1193	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	2e-04	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	2e-09
1194	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1195	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1196	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	1e-04	<NONE>	<NONE>	<NONE>
1197	X51890	Rhesus monkey interleukin-3 gene	1e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
1198	AE001421	falciparum chromosome 2, section 58 of 73 of the complete sequence	1e-04	<NONE>	<NONE>	<NONE>
1199	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1200	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1e-04	2576287	(Y15086) HepC protein [Cylindrotheca fusiformis]	4.7
1201	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	1e-04	3395673	(AB016623) RWC-3 [Oryza sativa]	0.14
1202	AF038035	Homo sapiens BRCA1-associated RING domain protein (BARD1) gene, exons 2 and 3	9e-05	<NONE>	<NONE>	<NONE>
1203	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	<NONE>	<NONE>	<NONE>
1204	AB012106	Brassica rapa mRNA for SRK45, complete cds	9e-05	<NONE>	<NONE>	<NONE>
1205	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	9e-05	<NONE>	<NONE>	<NONE>
1206	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	9e-05	1351553	HYPOTHETICAL LIPOPROTEIN MG348 PRECURSOR >gi\|1361668\|pir\|\|E64238 hypothetical protein MG348 - Mycoplasma genitalium (SGC3) >gi\|3844931	8.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1207	D50006	Human DNA for alpha-platelet-derived growth factor receptor, exon 6-10	9e-05	3063639	(AF056494) NADH dehydrogenase subunit 5 [Panorpa japonica]	5.1
1208	U50423	Human Down Syndrome region of chromosome 21, clone A41B8-1B7.	9e-05	124273	INHIBIN ALPHA CHAIN PRECURSOR bovine >gi\|163195 (M13273) inhibin A subunit [Bos taurus]	3.0
1209	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	4007782	(X72850) 2.4-dihydroxybenzoate monooxygenase [Sphingomonas sp.]	2.3
1210	AC005276	Homo sapiens clone fragment UWGC:gap3 from 7q31.3, complete sequence [Homo sapiens]	9e-05	1492075	(U60315) MC132L [Molluscum contagiosum virus subtype 1]	1.0
1211	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-05	2887423	(AB007884) KIAA0424 [Homo sapiens]	2e-10
1212	X77772	C.fuscus gamma-M2-1 crystallin mRNA.	9e-05	2072425	(U83115) non-lens beta gamma-crystallin like protein [Homo sapiens]	7e-25
1213	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1214	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1215	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1216	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1217	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1218	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1219	AF100694	Pontin52 mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1220	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1221	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	1722841	WNT-11 PROTEIN PRECURSOR (XWNT-11) clawed frog >gi\|439108 (L23542) maternal protein	9.9
1222	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1205991	(U35637) nebulin [Homo sapiens]	9.6
1223	AF024605	Homo sapiens serine protease-like protease Sequence 2 from patent US 5736377	8e-05	3242783	(AF055354) respiratory burst oxidase protein B	8.6
1224	Y13148	Rattus norvegicus mRNA for PAG608 gene	8e-05	2314243	(AE000616) alpha-ketoglutarate permease (kgtP)	8.1
1225	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	8e-05	1170586	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195) (KIAA0051) >gi\|627594\|pir\|\|A54854 Ras GTPase activating-related protein - human sapiens] >gi\|536844 (L33075) ras GTPase-activating-like protein [Homo sapiens]	7.8
1226	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi\|1085185\|pir\|\|S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi\|552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	3.5
1227	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	544353	F-SPONDIN PRECURSOR	3.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins).		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1228	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	483243	apolipoprotein B-100 - chicken (fragment)	3.4
1229	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	91207	proline-rich protein - mouse (fragment) musculus]	2.2
1230	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gi\|1066466	2.2
1231	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gi\|1066466	1.9
1232	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	2833647	(AF027972) flagelliform silk protein [Nephila clavipes]	1.6
1233	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	1163063	(Z49821) MYO2 [Saccharomyces cerevisiae]	0.90
1234	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1653488	(D90914) hypothetical protein	0.30
1235	M26510	Chicken nonmuscle myosin heavy chain (MHC) gene, complete cds.	8e-05	112159	plectin - rat	0.003
1236	U56402	Human chromatin structural protein homolog	8e-05	2088823	(AF003384) weak similarity to the peptidase family A2	1e-13
1237	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	437181	(U02289) GTPase-activating protein [Caenorhabditis elegans]	2e-17
1238	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	465983	HYPOTHETICAL 80.8 KD PROTEIN ZC21.4 IN CHROMOSOME III	8e-27

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1239	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1240	U83656	Rattus norvegicus NF-KB gene, promotor region	7e-05	3880858	(AL031633) predicted using Genefinder; cDNA EST yk304f12.5 comes from this gene [Caenorhabditis elegans]	9.3
1241	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-05	3080538	(AL022600) hypothetical protein	9.2
1242	X89398	H.sapiens ung gene for uracil DNA-glycosylase	7e-05	549700	HYPOTHETICAL 23.7 KD PROTEIN IN MDH1-VMA5 INTERGENIC REGION >gi\|539182\|pir\|\|S37908 hypothetical protein YKL083w - yeast (Saccharomyces cerevisiae) >gi\|486120 (Z28082) ORF YKL083w	1.8
1243	M83753	Bovine follicle stimulating hormone-beta subunit gene, complete cds.	7e-05	2398621	(AJ000342) DMBT1 protein, 5.8 kb transcript [Homo sapiens]	1.8
1244	M80829	Rat troponin T cardiac isoform gene, complete cds	5e-05	854065	(X83413) U88 [Human herpesvirus 6]	2e-08
1245	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	4e-05	120240	FLAGELLIN B2 PRECURSOR Methanococcus voltae >gi\|150063 (M72148) flagellin	5.2
1246	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1247	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1248	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rattus norvegicus				
1249	AF093268	homer-1c mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1250	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-05	2773226	(AF039716) Similar to protein kinase [Caenorhabditis elegans]	6.7
1251	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [Homo sapiens]	5.6
1252	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	121855	EXOGLUCANASE II PRECURSOR cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [Trichoderma reesei]	4.6
1253	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	3880516	(AL021572) similar to CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)	3.3
1254	M88299	Mouse brain-1 POU-domain protein, complete cds.	3e-05	1947048	(U66102) intimin [Escherichia coli]	3.0
1255	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3e-05	3122872	CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN) >gi\|1082650\|pir\|\|JC2522 nuclear autoantigen - human >gi\|805095 (U17989) GS2NA	2.8
1256	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - Thermus aquaticus >gi\|155083 (M84341) cytochrome c oxidase subunits precursor [Thermus thermophilus]	2.6
1257	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	2811015	SEGMENTATION POLARITY PROTEIN ENGRAILED >gi\|2076747 (U42429) engrailed [Anopheles gambiae] >gi\|2148918 (U42214) engrailed [Anopheles gambiae]	2.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1258	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-05	1657752	(U62325) FE65-like protein [Homo sapiens]	1.7
1259	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [Homo sapiens]	1.5
1260	U76523	Sambucus nigra lectin precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - Thermus aquaticus >gi\|155083 (M84341) cytochrome c oxidase subunits precursor [Thermus thermophilus]	1.1
1261	X91890	H.sapiens regulatory region of HOXA7 gene	3e-05	111013	Sxr (Bkm-homolog) sex-determining region protein - mouse	1.0
1262	L36936	Homo sapiens metase gene, partial cds.	3e-05	1944352	(D84239) IgG Fc binding protein [Homo sapiens]	0.99
1263	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	417782	SMP2 PROTEIN >gi\|320853\|pir\|\|S30911 SMP2 protein - yeast (Saccharomyces cerevisiae) gene [Saccharomyces cerevisiae]	0.89
1264	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	1708501	INTEGRIN ALPHA CHAIN-LIKE PROTEIN alpha Int1p [Candida albicans]	0.39
1265	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-05	1587031	cis-Golgi matrix protein GM130 [Rattus norvegicus]	0.20
1266	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-05	2072964	(U93569) putative p150 [Homo sapiens]	0.049

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					glycosylated and myristilated	
1267	Z96668	H.sapiens telomeric DNA sequence, clone 7PTEL001, read 7PTELOO001.seq	3e-05	542429	smaller surface antigen - Plasmodium falciparum >gi\|836640 (X76298) glycosylated and myristilated smaller surface antigen gallus] >gi\|1092178\|prf\|\|2023165B surface antigen	0.029
1268	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES...	2e-13
1269	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	2497677	ZYXIN (ZYXIN 2) sapiens] >gi\|1545954\|gnl\|PID\|e223417 (X95735) zyxin	2e-23
1270	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1e-05	<NONE>	<NONE>	<NONE>
1271	X16318	Canine mRNA for signal recognition particle 54k protein	1e-05	3122612	PITUITARY HOMEOBOX 3 (HOMEOBOX PROTEIN PITX3) >gi\|2645427 (AF005772) homeobox protein Pitx3 [Mus musculus]	4.4
1272	AB012105	Brassica rapa mRNA for SLG45, complete cds	1e-05	1652458	(D90905) DNA mismatch repair protein MutL [Synechocystis sp.]	0.62

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1273	U57843	Human phosphatidylinositol 3-kinase delta catalytic subunit mRNA, complete cds	1e-05	475909	(X67098) ORF1A [Homo sapiens]	0.22
1274	Z96569	H.sapiens telomeric DNA sequence, clone 2QTEL054, read 2QTELOO054.seq	1e-05	2137043	unknown protein - rabbit (fragment) cuniculus]	0.005
1275	AE000810	Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome	1e-05	3877579	(Z28271) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes... Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes...	6e-27
1276	AB012113	Homo sapiens gene for CC chemokine PARC precursor, complete cds	9e-06	<NONE>	<NONE>	<NONE>
1277	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-524I1 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	9e-06	<NONE>	<NONE>	<NONE>
1278	D86245	Human MHC (HLA) DRB intron 1 DNA, partial sequence	9e-06	1051253	(U37531) mucin apoprotein [Mus musculus]	1.3
1279	D79998	Human mRNA for KIAA0176 gene, partial cds	9e-06	2833253	HYPOTHETICAL PROTEIN KIAA0176 sapiens]	4e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z69635) Similarity to Yeast	
1280	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene, complete cds.	9e-06	3876090	uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-33
1281	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene, complete cds.	9e-06	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-34
1282	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1283	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1284	U66340	Human Rh blood group C antigen (RHCE) gene, exon 2, partial cds	8e-06	1707155	(U80837) F07E5.6 gene product [Caenorhabditis elegans]	9.6
1285	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-06	<NONE>	<NONE>	<NONE>
1286	M29930	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17.	4e-06	<NONE>	<NONE>	<NONE>
1287	L42103	Homo sapiens (subclone 5_d3 from P1 H25) DNA sequence.	3e-06	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1288	AF012244	cerberus-like (Cer-l) gene, complete cds	3e-06	<NONE>	<NONE>	<NONE>
1289	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1290	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1291	X85232	H.sapiens chromosome 3 sequences	3e-06	<NONE>	<NONE>	<NONE>
1292	M32674	Human platelet glycoprotein IIIa, exons 7, 8 and 9.	3e-06	<NONE>	<NONE>	<NONE>
1293	D16879	Human HepG2 3' region cDNA, clone hmd2a01	3e-06	998296	(U33484) ependymin [Hemiodus sp.]	5.6
1294	U18614	Lagothrix lagotricha interphotoreceptor retinoid-binding protein (IRBP) gene, intron 1, complete sequence	3e-06	1613846	(U71440) polyprotein [Rice tungro spherical virus]	5.0
1295	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-06	1477646	(U53204) plectin [Homo sapiens] >gi\|1477651 (U63610) plectin [Homo sapiens]	4.0
1296	AF016898	Homo sapiens B-ATF gene, complete cds	3e-06	1085177	reverse transcriptase - fruit fly reverse transcriptase [Drosophila yakuba]	3.0
1297	AB018490	Homo sapiens DNA, trinucleotide repeats region	3e-06	3876572	(Z81522) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) [Caenorhabditis elegans]	3.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1298	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-06	4240137	(AB020631) KIAA0824 protein [Homo sapiens]	2.7
1299	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1300	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1301	U60496	Glycine max actin (Soy86) gene, partial cds	3e-06	1730738	ACTIN-LIKE PROTEIN ARP5 Ynl2430p [Saccharomyces cerevisiae]	2e-05
1302	X14363	Yersinia pseudotuberculosis rplC, rplD, rplW, rplB and rpsS genes for ribosomal proteins L3, L4, L23, L2 and S19	3e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gi\|437926 (Z21677) ribosomal protein L2	2e-12
1303	Z34969	H.sapiens DNA for microsatellite polymorphism	2e-06	<NONE>	<NONE>	<NONE>
1304	X64707	H.sapiens BBC1 mRNA	1e-06	<NONE>	<NONE>	<NONE>
1305	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-524I1 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	1e-06	<NONE>	<NONE>	<NONE>
1306	J04058	Human electron transfer flavoprotein alpha-subunit mRNA, complete cds.	1e-06	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1307	L25647	Homo sapiens fibroblast growth factor receptor gene (located in the central MHC) signal peptide and consecutive exon	1e-06	1586734	mxcQ gene [Methylobacterium organophilum]	5.4
1308	L26261	Human MHC class III HLA-RP1 gene.	1e-06	1684985	(U20633) NADH dehydrogenase subunit [Neuwiedia veratrifolia]	1.8
1309	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	1e-06	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-17
1310	M10935	Human haptoglobin gene (alpha-2 allele), complete cds and haptoglobin-related gene, exon 1 and three Alu repeats.	6e-07	<NONE>	<NONE>	<NONE>
1311	AC002251	Homo sapiens (subclone 1_g6 from BAC H76) DNA sequence	4e-07	2144491	coagulation factor Xa (EC 3.4.21.6) precursor norvegicus]	4.2
1312	AF047717	Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds	4e-07	699196	(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]	1e-06
1313	U14417	Human Ral guanine nucleotide dissociation stimulator mRNA, partial cds.	4e-07	544402	GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) >gi\|321257\|pir\|\|S28415 guanine nucleotide dissociation stimulator ralGDS - mouse >gi\|193573 (L07924) guanine nucleotide dissociation stimulator [Mus musculus]	8e-08
1314	Z79027	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20G8	3e-07	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1315	U67167	intestinal mucin (MUC2) gene, promoter region and partial cds	3e-07	<NONE>	<NONE>	<NONE>
1316	AF086256	Homo sapiens full length insert cDNA clone ZD41C11	3e-07	<NONE>	<NONE>	<NONE>
1317	U67228	Human clone HS4.61 Alu-Ya5 sequence	3e-07	1938437	(U97003) contains similarity to C4-type zinc fingers and a ligand-binding domain of nuclear hormone receptors	2.3
1318	U94346	Human calpain-like protease (htra-3) mRNA, complete cds	3e-07	2911858	(AF047659) No definition line found [Caenorhabditis elegans]	0.39
1319	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	1e-07	<NONE>	<NONE>	<NONE>
1320	X13596	Bean DNA for glycine-rich cell wall protein GRP 1.8	1e-07	<NONE>	<NONE>	<NONE>
1321	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	1e-07	1326385	(U58751) C07G1.7 gene product [Caenorhabditis elegans]	8.0
1322	Z55905	H.sapiens CpG DNA, clone 71f4, forward read cpg71f4.ft1a .	1e-07	1076802	extensin-like protein - maize >gi\|600118 mays]	0.61
1323	X03541	Human mRNA of trk oncogene > :: gb\|I96186\|I96186 Sequence 23 from patent US 5734039	1e-07	325465	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1324	AF027766	Canis familiaris Y-linked zinc finger protein	1e-07	220643	(D10628) zinc finger protein [Mus musculus]	7e-08
1325	D13613	Bovine mRNA for rabphilin-3A, complete cds > :: dbj\|E07809\|E07809 cDNA encoding rabphilin-3A	1e-07	2822161	(AC004082) rab3 effector-like; 35% Similarity to AF007836 (PID:g2317778) [Homo sapiens]	6e-11

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for c-			(J04169) gag-onc fusion protein	
1326	X57110	cbl proto-oncogene	1e-07	323270	[Cas NS1 retrovirus]	3e-14
1327	X57110	Human mRNA for c-cbl proto-oncogene	1e-07	115855	PROTO-ONCOGENE C-CBL human >gi\|29731 (X57110) c-cbl protein [Homo sapiens]	4e-19
1328	AC001178	Homo sapiens (subclone 2_g12 from BAC H94) DNA sequence	4e-08	<NONE>	<NONE>	<NONE>
1329	U11866	Human interleukin-8 receptor type B (IL8RB) gene, promoter and exons 1-6	4e-08	<NONE>	<NONE>	<NONE>
1330	AC001225	Homo sapiens (subclone 2_e6 from BAC H94) DNA sequence	4e-08	478184	histone H1 II-1 (clone L95) - midge	6.5
1331	M73837	Human modulator recognition factor 2 (MRF-2) mRNA, complete cds.	4e-08	141448	HYPOTHETICAL 32.6 KD PROTEIN IN TRANSPOSON TN4556 >gi\|80758\|pir\|\|JQ0428 hypothetical 32.6K protein - Streptomyces fradiae transposon Tn4556	4.7
1332	AC006164	Homo sapiens clone UWGC:y28gap from 6p21, complete sequence [Homo sapiens]	4e-08	2580578	(AF000996) ubiquitous TPR motif, Y isoform [Homo sapiens]	1.2
1333	X01060	Human mRNA for transferrin receptor	4e-08	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA 11) - rabbit	0.61
1334	Y10697	H.sapiens INE2 mRNA	4e-08	124909	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR) >gi\|186555 sapiens]	0.14
1335	U60416	Rattus norvegicus myr 6 myosin heavy chain mRNA, complete cds	4e-08	102189	myosin I, high molecular weight - Acanthamoeba sp	3e-08

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1336	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	4e-08	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-28
1337	AE000213	Escherichia coli K-12 MG1655 section 103 of 400 of the complete genome	4e-08	3294172	(AL022325) fF27C3.1.1 (protein similar to C. elegans protein B0035.16) (isoform 1) [Homo sapiens]	2e-67
1338	D89821	Mus musculus mRNA for RhoM, complete cds	2e-08	3024539	RHO-RELATED GTP-BINDING PROTEIN RHOD (RHO-RELATED PROTEIN HP1) (RHOHP1) sapiens]	1e-04
1339	U74382	Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1340	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	1e-08	<NONE>	<NONE>	<NONE>
1341	L21936	Human succinate dehydrogenase flavoprotein subunit	1e-08	3201678	(AF060886) adenine phosphoribosyltransferase [Leishmania tarentolae]	4.0
1342	AB009777	Homo sapiens gene for osteonidogen, promoter region	1e-08	479388	tritin - wheat >gi\|391929\|gnl\|PID\|d1003454	2.2
1343	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.9
1344	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.7
1345	AC000980	Homo sapiens (subclone 1_g2 from P1 H31) DNA sequence	1e-08	439877	(L27428) reverse transcriptase [Homo sapiens]	1.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1346	U48734	Human non-muscle alpha-actinin mRNA, complete cds	1e-08	168237	(M76546) hydroxyproline-rich protein [Helianthus annuus]	0.19
1347	M76724	Human leukocyte adhesion receptor alpha subunit	1e-08	1177607	(X92485) pval [Plasmodium vivax]	0.19
1348	AF067959	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds	1e-08	3165574	(AF067942) No definition line found [Caenorhabditis elegans]	0.15
1349	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	1e-08	2072964	(U93569) putative p150 [Homo sapiens]	0.001
1350	X57103	Human h-lys gene for lysozyme (upstream region)	7e-09	<NONE>	<NONE>	<NONE>
1351	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-09	231629	BILE-SALT-ACTIVATED LIPASE PRECURSOR ESTER LIPASE) (STEROL ESTERASE) (CHOLESTEROL ESTERASE) salt-activated lipase [Homo sapiens] sapiens]	0.22
1352	L34741	Aplysia californica prohormone convertase (PC2) mRNA, complete cds.	5e-09	322054	cytochrome-c oxidase (EC 1.9.3.1) chain II precursor - Synechocystis sp. (PCC 6803) >gi\|581739 sp.]	5.0
1353	AF052959	Homo sapiens type XV collagen (COL15A1) gene, exon 6	4e-09	131269	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi\|72708\|pir\|\|QJLV6A photosystem II chlorophyll a-binding protein psbB - liverwort (Marchantia polymorpha) chloroplast >gi\|11700	1.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					POSSIBLE AGMATINASE (AGMATINE UREOHYDROLASE) (AUH) (PROCLAVAMINIC ACID AMIDINO HYDROLASE) >gi\|1361423\|pir\|\|S57669 Proclavaminic acid amidino hydrolase - Streptomyces clavuligerus >gi\|295171 Proclavaminic acid amidino hydrolase [Streptomyces clavuligerus] >gi\|1586122\|prf\|\|2203286B proclavaminic acid amidino hydrolase [Streptomyces clavuligerus]	
1354	L15470	Streptomyces clavuligerus (NRRL 3585) clavulanic acid biosynthesis protein (cla) gene, complete cds and clavaminate synthase 2 (cs2) gene, partial cds.	4e-09	586028		4e-13
1355	AB002302	Human mRNA for KIAA0304 gene, complete cds	2e-09	131600	GENERAL SECRETION PATHWAY PROTEIN L product [Klebsiella pneumoniae] >gi\|149311 (M32613) pulL	2.5
1356	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	1e-09	<NONE>	<NONE>	<NONE>
1357	AB002302	Human mRNA for KIAA0304 gene, complete cds	1e-09	2224549	(AB002302) KIAA0304 [Homo sapiens]	5.0
1358	D85731	Homo sapiens HSPA1L gene for Heat shock protein 70 testis variant, 5'UTR, partial sequence	1e-09	1389766	(U58658) unknown [Homo sapiens]	1.3
1359	AF064483	Homo sapiens natural resistance-associated macrophage protein 2 (NRAMP2) gene, exon 17, alternatively spliced non-IRE form, complete cds	8e-10	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.72

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1360	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	6e-10	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-21
1361	M26220	African green monkey origin of replication	5e-10	2143455	gene DMR-N9 protein - mouse (fragment)	8.8
1362	Z78006	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA7F10	4e-10	2072977	(U93574) putative p150 [Homo sapiens]	0.005
1363	U82303	Homo sapiens unknown protein mRNA, partial cds	2e-10	1825711	(U88183) similar to the immunoglobulin superfamily, most similar to nerual cell adhesion proteins [Caenorhabditis elegans]	0.031
1364	AF079764	Drosophila melanogaster enhancer of polycomb	2e-10	3757890	(AF079764) enhancer of polycomb [Drosophila melanogaster]	1e-10
1365	L24123	Homo sapiens NRF1 protein (NRF1) mRNA.	2e-10	3004573	(AC004520) similar to NFE2-related transcription factors; similar to I48694 (PID:g2137676) [Homo sapiens]	4e-53
1366	M91454	Orangutan alpha-globin gene duplicate region.	1e-10	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi\|1085185\|pir\|\|S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi\|552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	6.0
1367	D87117	House mouse; Musculus domesticus brain mRNA for SAP102, complete cds	6e-11	473912	(L31961) phosphoprotein [Mus cookii]	2.2
1368	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1369	AC001002	(subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1370	AB007874	Homo sapiens KIAA0414 mRNA, partial cds	5e-11	<NONE>	<NONE>	<NONE>
1371	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1372	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1373	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1374	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1375	Z21852	H.sapiens mRNA for HERV-K long terminal repeat	5e-11	419481	gag polyprotein - human endogenous virus S71	4.6
1376	AB007928	Homo sapiens mRNA for KIAA0459 protein, partial cds	5e-11	2947238	(AF051782) diaphanous 1 [Homo sapiens]	2.8
1377	D87117	House mouse; Musculus domesticus brain mRNA for SAP102, complete cds	5e-11	473912	(L31961) phosphoprotein [Mus cookii]	1.8
1378	AJ131501	Homo Sapiens DNA sequence between two AML1 gene promoters, 6423 BP	5e-11	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.20
1379	M27826	Human endogenous retroviral protease mRNA, complete cds.	5e-11	88558	retroviral proteinase-like protein - human	0.002

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1380	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	5e-11	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-30
1381	Z22784	M.musculus troponin I gene.	3e-11	3892202	(AF072889) transcription repressor brain factor 2	0.053
1382	AB007880	Homo sapiens KIAA0420 mRNA, complete cds	2e-11	<NONE>	<NONE>	<NONE>
1383	AF020361	9 Homo sapiens BAX gene, exon 6, partial sequence	2e-11	<NONE>	<NONE>	<NONE>
1384	L35600	Homo sapiens DNA sequence.	2e-11	1174952	GLYCOPROTEIN D PRECURSOR gD [Bovine herpesvirus 1]	0.25
1385	U21943	Human organic anion transporting polypeptide	2e-11	2738223	(U95011) brain-specific organic anion transporter	9e-19
1386	U90878	Homo sapiens carboxyl terminal LIM domain protein	2e-11	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-23
1387	U31929	Human orphan nuclear receptor (DAX1) gene, complete cds	6e-12	<NONE>	<NONE>	<NONE>
1388	M25828	Human von Willebrand factor gene, exon 1, 2, and 3, and three Alu repetitive elements.	6e-12	<NONE>	<NONE>	<NONE>
1389	AB020648	Homo sapiens mRNA for KIAA0841 protein, partial cds	3e-12	<NONE>	<NONE>	<NONE>
1390	Z15026	H.sapiens genes for tumor necrosis factor (Tnfa) and lymphotoxine (Tnfb)	2e-12	<NONE>	<NONE>	<NONE>
1391	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	2e-12	<NONE>	<NONE>	<NONE>
1392	Z47046	Human cosmid QLL2C9 from Xq28	2e-12	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens flow-sorted				
1393	Z79007	chromosome 6 HindIII fragment, SC6pA20E2	2e-12	106322	hypothetical protein (L1H 3' region) - human	1.5
1394	U34377	Human tyrosine kinase TXK (txk) gene, exon 13.	1e-12	151484	(M55524) ORF 4; putative [Pseudomonas aeruginosa]	4.3
1395	D70845	Mus musculus apg-1 gene for novel member of heat shock protein 110, promoter region	1e-12	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.5
1396	M63978	Human vascular endothelial growth factor gene, exon 8.	1e-12	3982737	(AF069731) calmodulin-dependent protein kinase II beta M isoform [Rattus norvegicus]	0.083
1397	U60266	Homo sapiens lysosomal alpha-mannosidase (manB) mRNA, complete cds	8e-13	<NONE>	<NONE>	<NONE>
1398	Z68297	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	5e-34
1399	Z68297	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	3e-38
1400	Z68885	Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.	6e-13	<NONE>	<NONE>	<NONE>
1401	X76104	H.sapiens DAP-kinase mRNA	6e-13	2911154	(AB007143) ZIP-kinase [Mus musculus]	0.007
1402	Z78668	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA13G4	5e-13	106322	hypothetical protein (L1H 3' region) - human	2e-06
1403	L35600	Homo sapiens DNA sequence.	3e-13	3184290	(AC004136) hypothetical protein [Arabidopsis thaliana]	1.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cloning vector				
1404	AF090452	pKODT complete sequence	2e-13	3876730	(Z49966) F35C11.4 [Caenorhabditis elegans]	7.8
1405	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	2e-13	419481	gag polyprotein - human endogenous virus S71	3.4
1406	AF005219	Homo sapiens transcription factor HOXD13	2e-13	2822166	(AC004080) transcription factor HOXA13 [Homo sapiens]	5e-09
1407	AB018301	Homo sapiens mRNA for KIAA0758 protein, partial cds	2e-13	3882237	(AB018301) KIAA0758 protein [Homo sapiens]	1e-23
1408	D70845	Mus musculus apg-1 gene for novel member of heat shock protein 110, promoter region	1e-13	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.1
1409	AG000691	Homo sapiens genomic DNA, 21q region, clone: T171BG33	8e-14	930045	(X15332) alpha-1 (III) collagen [Homo sapiens]	3e-04
1410	D30785	Mouse mRNA for neuropsin, complete cds	8e-14	3559978	(AJ005641) serine protease [Rattus rattus]	2e-12
1411	U32710	Haemophilus influenzae Rd section 25 of 163 of the complete genome	8e-14	4106673	(AL035064) queuine trna-ribosyltransferase [Schizosaccharomyces pombe]	2e-38
1412	AG000886	Homo sapiens genomic DNA, 21q region, clone: 64E11X19	7e-14	1363925	hypothetical protein 2 - North American opossum (fragment) >gi\|897721 (Z48955) ORF-2, putative RT [Didelphis virginiana]	1.1
1413	Z62664	H.sapiens CpG DNA, clone 71d11, forward read cpg71d11.ft1a .	7e-14	3953461	(AC002328) F20N2.6 [Arabidopsis thaliana]	0.085
1414	AB014532	Homo sapiens mRNA for KIAA0632 protein, partial cds	7e-14	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.040

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1415	Z96478	H.sapiens telomeric DNA sequence, clone 20PTEL004, read 20PTELOO004.seq	7e-14	2981631	(AB012223) ORF2 [Canis familiaris]	2e-04
1416	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1417	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1418	AF033349	Homo sapiens MLL gene breakpoint cluster region, intron 1, partial sequence	3e-14	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	9.3
1419	AC001526	Homo sapiens (subclone 4_f6 from P1 H54) DNA sequence	3e-14	99861	extensin - almond >gi\|20420 (X65718) extensin	9.2
1420	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-14	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.15
1421	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-14	3913573	EPHRIN-A2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 6) (LERK-6) sapiens] >gi\|2924761 (AC004258) EPL6_HUMAN [Homo sapiens]	8.7
1422	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-15	119040	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K) >gi\|74142\|pir\|\|Q1AD25 early E1B 21K protein II - human adenovirus 5 >gi\|58489 (X02996) mRNA 5 first reading frame [Human adenovirus type 5] adenovirus type 5] >gi\|209797 (J01969) 21 kD protein	1.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					transcription factor GATA-4,	
1423	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-15	477102	retinoic acid-inducible - mouse >gi\|293345 (M98339) GATA-binding transcription factor [Mus musculus]	0.57
1424	AB012223	Canis familiaris LINE 1 element ORF2 mRNA, complete cds	8e-15	92385	hypothetical protein - rat (fragment)	0.003
1425	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1426	X12433	Human pHS1-2 mRNA with ORF homologous to membrane receptor proteins	3e-15	422532	collagen alpha 3(IV) chain - sea urchin	8.9
1427	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	1353143	PROBABLE NUCLEAR HORMONE RECEPTOR E02H1.7 >gi\|3875431\|gnl\|PID\|e1344980 (Z47075) similar to Zinc finger, C4 type (two domains) [Caenorhabditis elegans]	5.0
1428	Z69651	Human DNA sequence from cosmid L75B9, Huntington's Disease Region, chromosome 4p16.3	3e-15	403460	(L24521) transformation-related protein [Homo sapiens]	0.60
1429	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	108750	Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine >gi\|440 (X62916) anti-testosterone antibody [Bos taurus]	1.1
1430	X83299	H.sapiens SMA3 mRNA	2e-15	671530	(X83299) SMA3 gene product [Homo sapiens]	0.32
1431	U01877	Human p300 protein mRNA, complete cds. > :: gb\|I62297\|I62297 Sequence 1 from patent US 5658784	2e-15	3024341	E1A-ASSOCIATED PROTEIN P300	0.019

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 45.1 KD	
1432	X16516	Mouse MHC (Qa) Q2 k gene for class I antigen, exons 4-8	1e-15	2496897	PROTEIN C16C10.6 IN CHROMOSOME III >gi\|3874384\|gnl\|PID\|e1344078 EST EMBL:C08256 comes from this gene; cDNA EST EMBL:C09941 comes from this gene; cDNA EST yk340a10.3 comes from this gene; cDNA EST yk340a10.5 comes from this gene [Ca...	7e-08
1433	M74165	Chicken tensin mRNA, complete cds.	1e-15	283920	tensin - chicken >gi\|212752 (M74165) tensin	2e-19
1434	X71893	H.sapiens gene for immunoglobulin kappa light chain variable region O4 and O5	9e-16	<NONE>	<NONE>	<NONE>
1435	U05227	Human Rar protein mRNA, complete cds.	9e-16	3036779	(Z84479) match: multiple proteins; match: O00407 Q12829 P22127 P36861 Q40219; match: P70550 Q41022 P22125 Q08155 P35286; match: P51148 P51147 P35293 P36861 P35289; match: P35284 Q40217 P51152 P51157 P51158; match: Q41022	3e-06
1436	M23404	Chicken erythrocyte anion transport protein (band3) mRNA, complete cds.	9e-16	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	1e-28
1437	X16145	Rat mRNA for liver a-L-Fucosidase (EC 3.2.1.51)	9e-16	67502	alpha-L-fucosidase (EC 3.2.1.51) 1 precursor, tissue - human >gi\|178409 (M29877) alpha-L-fucosidase precursor (EC 3.2.1.5) [Homo sapiens]	2e-29
1438	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-16	<NONE>	<NONE>	<NONE>
1439	AF076981	Mus musculus brain mitochondrial carrier protein BMCP1 (Bmcp1) mRNA, complete cds	8e-16	3851540	(AF078544) brain mitochondrial carrier protein-1 [Homo sapiens]	2e-13

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens MN/CA9			!!!! ALU SUBFAMILY J	
1440	Z54349	GENE	5e-16	728831	WARNING ENTRY	0.002
1441	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	3e-16	309123	(M35526) complement component C5D [Mus musculus]	3.1
1442	X64587	M.musculus mRNA for splicing factor U2AF (65 kD)	3e-16	2143767	glycoprotein - rat >gi\|986943 (L08134) glycoprotein [Rattus norvegicus] norvegicus]	0.003
1443	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	3e-16	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-20
1444	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22 Contains ESTs, complete sequence [Homo sapiens]	1e-16	<NONE>	<NONE>	<NONE>
1445	M58318	Homo sapiens ala gene.	1e-16	<NONE>	<NONE>	<NONE>
1446	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-16	1552584	(Z80233) hypothetical protein Rv0029	1.3
1447	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	9e-17	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	2e-20
1448	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-17	<NONE>	<NONE>	<NONE>
1449	M76762	Mus musculus ribosomal protein (Ke 3) gene, exons 1 to 5, and complete cds.	1e-17	1073048	pupR protein - Pseudomonas putida >gi\|525260	0.36
1450	D50561	Human DNA, replication enhancing element (REE1)	4e-18	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.78
1451	D16431	Human mRNA for hepatoma-derived growth factor, complete cds	4e-18	3242079	(AJ006984) proline-rich protein	0.018

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1452	AF088983	Mus musculus heat shock protein hsp40-3 mRNA, complete cds	4e-18	3873707	(Z73102) Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene [Caenorhabditis elegans]	9e-25
1453	U60205	Human methyl sterol oxidase (ERG25) mRNA, complete cds	3e-18	<NONE>	<NONE>	<NONE>
1454	AF038177	Homo sapiens clone 23899 mRNA sequence	1e-18	1360775	G protein-coupled receptor 74 - equine herpesvirus 2 >gi\|695246 (U20824) G protein-coupled receptor [Equine herpesvirus 2]	5.1
1455	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-21
1456	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-22
1457	U34374	Human tyrosine kinase TXK (txk) gene, exons 9 and 10.	1e-19	<NONE>	<NONE>	<NONE>
1458	AB006969	Homo sapiens hGAA1 mRNA, complete cds	1e-19	4151809	(AF102855) synaptic SAPAP-interacting protein Synamon	0.19
1459	AB002293	Human mRNA for KIAA0295 gene, partial cds	1e-19	2224531	(AB002293) KIAA0295 [Homo sapiens]	6e-17
1460	Z59664	H.sapiens CpG DNA, clone 168f9, reverse read cpg168f9.rt1a .	5e-20	3880251	(Z82055) predicted using Genefinder	6.5
1461	M73837	Human modulator recognition factor 2 (MRF-2) mRNA, complete cds.	5e-20	284313	modulator recognition factor 2 - human factor 2 [Homo sapiens]	0.019

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1462	U24267	Human pyrroline-5-carboxylate dehydrogenase	5e-20	2506350	DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR (P5C DEHYDROGENASE) >gi\|1353248 sapiens] >gi\|1353250 (U24267) pyrroline 5-carboxylate dehydrogenase [Homo sapiens] >gi\|1589585\|prf\|\|2211355A Delta1-pyrroline-5-carboxylate dehydrogenase [Homo sapiens]	5e-04
1463	U13262	Mus musculus myelin gene expression factor	4e-20	536926	(U13262) myelin gene expression factor [Mus musculus]	3e-07
1464	U13262	Mus musculus myelin gene expression factor	4e-20	3126878	(AF061832) M4 protein deletion mutant [Homo sapiens]	1e-08
1465	Z61239	H.sapiens CpG DNA, clone 48f10, forward read cpg48f10.ft1a .	4e-20	1669601	(D88747) AR401 [Arabidopsis thaliana]	8e-19
1466	U89915	Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds	1e-20	3462455	(U89915) junctional adhesion molecule [Mus musculus]	7e-11
1467	AF029071	Gallus gallus p52 pro-apototic protein mRNA, complete cds	7e-22	2599492	(AF029071) p52 pro-apototic protein [Gallus gallus]	1e-15
1468	M25636	Figure 4. Nucleotide sequence of the pKS36 1.797 kb insert.	6e-22	1196398	(M21305) unknown protein [Homo sapiens]	0.65
1469	AB020655	Homo sapiens mRNA for KIAA0848 protein, complete cds	6e-22	4240325	(AB020725) KIAA0918 protein [Homo sapiens]	1e-19

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROCOLLAGEN ALPHA	
1470	S80935	chorionic gonadotropin beta 1 (CG beta 1) subunit	5e-22	115310	I(IV) CHAIN PRECURSOR >gi\|84917\|pir\|\|A31893 collagen alpha 1(IV) chain precursor - fruit fly (Drosophila melanogaster) melanogaster] >gi\|157078 (M96575) type IV collagen pro-collagen [Drosophila melanogaster]	0.027
1471	AF053066	Homo sapiens microsatellite D5S2926 sequence	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-04
1472	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	2e-22	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi\|2576335 (U55177) CAH-Z [Danio rerio]	5e-14
1473	AF064250	Gallus gallus ubiquitin specific protease 66	2e-22	2736064	(AF016107) ubiquitin specific protease 41 [Gallus gallus]	7e-37
1474	AF030880	Homo sapiens pendrin (PDS) mRNA, complete cds	2e-22	729367	DRA PROTEIN (DOWN-REGULATED IN ADENOMA) >gi\|2135020\|pir\|\|A47456 down-regulated in adenoma (DRA) - human >gi\|291964 (L02785) Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transcr. activ. domain 620-640,; homeobox motif 653-676 [Homo sapiens]	4e-53
1475	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	<NONE>	<NONE>	<NONE>
1476	X57398	Human mRNA for pM5 protein	3e-23	107350	Pm5 protein - human >gi\|1335273\|gnl\|PID\|e36241	1e-04
1477	AB010998	Rattus norvegicus PAD-R11 mRNA for Peptidylarginine deiminase type I, complete cds	2e-23	<NONE>	<NONE>	<NONE>
1478	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	9.8
1479	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	8.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens MLL-				
1480	AF024541	AF4 fusion protein mRNA, partial cds	2e-23	2136142	serine/proline-rich FEL protein, splice form 1 - human	1e-20
1481	L13773	Human AF-4 mRNA, complete cds.	2e-23	3063962	(AF031404) MLL-AF4 fusion protein [Homo sapiens]	1e-20
1482	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-24	<NONE>	<NONE>	<NONE>
1483	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	8e-24	1658503	(U75467) Atu [Drosophila melanogaster]	2e-37
1484	D17076	Human HepG2 partial cDNA, clone hmd5a09m5	7e-24	<NONE>	<NONE>	<NONE>
1485	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-24	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi\|416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	7e-10
1486	M11167	Human 28S ribosomal RNA gene.	2e-24	3875481	(Z81054) predicted using Genefinder; Similarity to UDP-glucoronosyltransferases	5.1
1487	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-24	549173	USP1 PROTEIN PRECURSOR >gi\|169623	1.2
1488	AB003468	Cloning vector pAP3neo DNA, complete sequence	2e-24	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.058
1489	X03541	Human mRNA of trk oncogene > :: gb\|I96186\|I96186 Sequence 23 from patent US 5734039	2e-24	325465	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1490	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	2e-24	225047	reverse transcriptase related protein [Homo sapiens]	4e-12
1491	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	2e-24	2078282	(U95760) Sno [Drosophila melanogaster]	2e-41
1492	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-25	2623773	(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	8.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1493	AB002405	Homo sapiens mRNA for LAK-4p, complete cds	8e-25	2496822	HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X >gi\|746502 (U23516) B0416.1 gene product [Caenorhabditis elegans]	9e-11
1494	K03002	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A.	8e-25	1514614	(X92842) nuclear protein [Mus musculus]	1e-13
1495	U61232	Human tubulin-folding cofactor E mRNA, complete cds	7e-25	1465772	(U61232) cofactor E [Homo sapiens]	2e-05
1496	U10245	Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.	5e-25	1353239	(U10245) putative RNA helicase A [Arabidopsis thaliana]	1e-37
1497	X89211	H.sapiens DNA for endogenous retroviral like element	3e-25	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	5e-06
1498	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	3e-25	2072961	(U93568) putative p150 [Homo sapiens]	5e-16
1499	X82895	H.sapiens mRNA for DLG2	2e-25	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS, LARGE HOMOLOG 2)	1e-34
1500	M36654	Mouse homeo box 2.6 (Hox-2.6) mRNA, complete cds.	9e-26	3323169	(AE001255) T. pallidum predicted coding region TP0854	1.9
1501	L36315	Mus musculus (clone pMLZ-1) zinc finger protein	9e-26	1806134	(Z67747) zinc finger protein [Mus musculus]	4e-05
1502	AB018281	Homo sapiens mRNA for KIAA0738 protein, complete cds	9e-26	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-07
1503	AF017433	Homo sapiens putative transcription factor CR53	9e-26	3219985	ZINC FINGER PROTEIN ZFP-29	1e-17

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1504	AC001225	(subclone 2_e6 from BAC H94) DNA sequence	8e-26	2653713	(U91823) small S protein [Hepatitis B virus]	4.3
1505	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-26	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	3.4
1506	X94912	H.sapiens Pr22 gene	3e-26	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY.	4e-09
1507	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-26	<NONE>	<NONE>	<NONE>
1508	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-26	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	8.7
1509	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.14
1510	AG001212	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	9e-27	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.012
1511	AF027131	Mus musculus mucin glycoprotein MUC3 mRNA, partial cds	9e-27	2589172	(U76551) mucin Muc3 [Rattus norvegicus]	2e-14
1512	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	5e-27	1438534	(U49057) rA9 [Rattus norvegicus]	1e-04
1513	J03764	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9.	3e-27	<NONE>	<NONE>	<NONE>
1514	Z78160	M.musculus partial cochlear mRNA (clone 28D2)	3e-27	1490362	(Z78160) unknown [Mus musculus]	2e-05
1515	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.rt1a .	3e-27	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	1e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1516	L35659	(subclone H8 6_h6 from P1 35 H5 C8) DNA sequence.	1e-27	<NONE>	<NONE>	<NONE>
1517	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	1644471	(U72686) odorant receptor 4 [Danio rerio]	7.5
1518	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2738388	(AF003534) hypothetical protein 004L [Chilo iridescent virus]	6.7
1519	AB009271	Homo sapiens gene for BCNT, partial cds	1e-27	3880909	(AL032636) Y40B1B.3 [Caenorhabditis elegans]	4.6
1520	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.85
1521	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	121805	ENDOGLUCANASE A PRECURSOR	0.58
1522	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3722000	(AF035323) survival motor neuron protein [Bos taurus]	0.10
1523	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.083
1524	AF074382	Homo sapiens IkB kinase gamma subunit	1e-27	3641280	(AF074382) IkB kinase gamma subunit [Homo sapiens]	0.041
1525	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1526	L78778	Homo sapiens (subclone 2_e10 from P1 H49) DNA sequence	1e-27	225047	reverse transcriptase related protein [Homo sapiens]	2e-09
1527	L03427	Human zinc finger protein basonuclin mRNA, complete cds.	1e-27	1488275	(U59694) zinc finger protein basonuclin [Homo sapiens]	9e-22
1528	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	4e-28	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	2e-04

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1529	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.rt1a .	4e-28	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	7e-11
1530	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	4e-28	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi\|2576335 (U55177) CAH-Z [Danio rerio]	5e-21
1531	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-28	1351839	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) >gi\|930358 taurus]	3e-27
1532	AF016591	Homo sapiens survival motor neuron pseudogene, complete sequence	3e-28	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-08
1533	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	2.5
1534	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.004
1535	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi\|416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	6e-04
1536	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	9e-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1537	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1538	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-09
1539	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1540	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1541	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-11
1542	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb\|Z34465 from Zea mays. [Arabidopsis thaliana]	8e-12
1543	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1544	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1545	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1546	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1547	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1548	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1549	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1550	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1551	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1552	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1553	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1554	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1555	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1556	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1557	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1558	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1559	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1560	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1561	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1562	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1563	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1564	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1565	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1566	M87708	Human simple repeat polymorphism.	1e-28	<NONE>	<NONE>	<NONE>
1567	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1568	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	(AL008985) similar to tammm B; cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi\|3924881\|gnl\|PID\|e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	3.0
1569	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi\|416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.66

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AL008585) similar to laminin B, cDNA EST yk450d8.5 comes	
1570	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi\|3924881\|gnl\|PID\|e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.65
1571	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1572	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1573	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	0.45
1574	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2498937	SPERMATOPHORIN SP23 PRECURSOR mealworm >gi\|161725 (M92928) structural protein	0.33
1575	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1492050	(U60315) MC107L [Molluscum contagiosum virus subtype 1]	0.18
1576	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.088
1577	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.018
1578	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.016

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DEHYDRIN DHN3	
1579	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	>gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.012
1580	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.010
1581	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1582	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi\|416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.002
1583	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1584	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1585	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1586	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1587	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.001
1588	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1589	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1590	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1591	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	2e-04
1592	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-04
1593	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1594	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-05
1595	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1596	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1597	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	9e-06
1598	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	6e-06
1599	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-06
1600	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	544357	RNA-BINDING PROTEIN FUS/TLS protein [human, Peptide, 526 aa] [Homo sapiens]	4e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1601	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1602	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1603	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	9e-07
1604	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	8e-07
1605	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi\|416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	7e-07
1606	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	6e-07
1607	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-07

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1608	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	3e-07
1609	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1610	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1611	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	7e-08
1612	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-08
1613	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	6e-09

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1614	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-09
1615	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	4e-09
1616	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	7e-10
1617	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	6e-10
1618	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1619	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	4e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1620	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-10
1621	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	5e-11
1622	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-12
1623	AF032896	Petromyzon marinus polyadenylate binding protein	1e-28	1082703	polyadenylate binding protein II human	2e-27
1624	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.013
1625	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	2133579	spermatophorin Sp23 - yellow mealworm molitor]	6e-04
1626	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	3876465	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gen...	9e-06
1627	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-29	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	2e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ADP-RIBOSYLATION	
1628	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	728883	FACTOR 3 fruit fly (Drosophila melanogaster) >gi\|507234 (L25063) ADP ribosylation factor 3 [Drosophila melanogaster]	0.016
1629	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	544357	RNA-BINDING PROTEIN FUS/TLS protein [human, Peptide, 526 aa] [Homo sapiens]	2e-07
1630	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-08
1631	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-29	1168287	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) dehydrogenase precursor - rat Acyl-CoA dehydrogenase [Rattus norvegicus]	6e-37
1632	Y07660	M.tuberculosis accBC gene	4e-29	2113935	(Z95556) accD1 [Mycobacterium tuberculosis]	3e-47
1633	X55367	Human alpha-satellite DNA from clone pTRA-2.	1e-29	<NONE>	<NONE>	<NONE>
1634	L81866	Homo sapiens (subclone 1_f1 from P1 H54) DNA sequence	1e-29	<NONE>	<NONE>	<NONE>
1635	S75940	{Alu repeats, clone 52H10} [human, colonic mucosa, Genomic, 943 nt]	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-07
1636	AB001907	Homo sapiens PACE4 gene, exon 13	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	2e-09
1637	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	5e-30	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1638	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-30	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	3e-10
1639	M27072	Xenopus laevis poly(A)-binding protein (ABP-EF) mRNA, complete cds.	4e-30	1352709	POLYADENYLATE-BINDING PROTEIN polyadenylate-binding protein - African clawed frog laevis]	5e-21
1640	X58386	B.taurus mRNA for bovine vacuolar ATPase subunit A	2e-30	2773154	(AF039573) abscisic acid- and stress-inducible protein	4.3
1641	Y07660	M.tuberculosis accBC gene	1e-30	2113935	(Z95556) accD1 [Mycobacterium tuberculosis]	4e-47
1642	AJ236940	Sus scrofa mRNA for hypothetical protein (5'; clone 7C4)	4e-31	4102021	(AF007561) delta 6-desaturase [Borago officinalis]	7.4
1643	AF039400	Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) mRNA, complete cds	2e-31	3721912	(AB017156) gob-5 [Mus musculus]	7e-08
1644	L77036	Homo sapiens (subclone 5_d9 from P1 H19) DNA sequence.	1e-31	461663	BOMBYXIN B-2 HOMOLOG PRECURSOR silkmoth >gi\|217385\|gnl\|PID\|d1003528 (D13924) Samia bombyxin homolog B-2 [Samia cynthia]	1.1
1645	X61971	H.sapiens mRNA for macropain subunit delta	1e-31	296734	(X61971) macropain subunit delta [Homo sapiens]	3e-06
1646	L00016	human mitochondrial trnas and partial proteins 4 & 5; histidyl-, seryl-, leucyl-trna genes; urf4 and urf5 (partial).	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1647	M17887	Human acidic ribosomal phosphoprotein P2 mRNA, complete cds.	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1659	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	6e-34	3395443	(AC004683) putative ammonium transporter, 3' partial	4.7
1660	AF013988	Homo sapiens serine protease mRNA, complete cds	4e-34	2507226	PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (R-PTP-EPSILON) >gi\|1439605 (U62387) protein tyrosine phosphatase-e [Mus musculus]	3.2
1661	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	2e-34	104757	LEP100 protein precursor - chicken >gi\|212254 gallus]	1.6
1662	AJ233632	Homo sapiens endogenous retroviral sequence ERV-L pol gene, clone ERV-L Human6	2e-34	3860513	(AJ233597) reverse transcriptase [Mus famulus]	4e-10
1663	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	8e-35	2947070	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]	2.3
1664	X17206	Human mRNA for LLRep3	3e-35	730652	40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) >gi\|1085158\|pir\|\|S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) melanogaster] >gi\|515972 (U01335) ribosomal protein S2	2e-10
1665	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	3e-35	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	2e-16
1666	U62801	Human protease M mRNA, complete cds	2e-35	3929231	(AF091247) potassium channel [Rattus norvegicus]	1.0
1667	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	1e-35	2738915	(AF020760) serine protease [Homo sapiens]	9e-14

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1668	Z93943	sequence from cosmid U235H3 on chromosome X	8e-36	1196432	(M22333) unknown protein [Homo sapiens]	3e-10
1669	X06778	Rabbit 18S rRNA	7e-36	118588	DEHYDRIN DHN3 >gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.011
1670	AB007962	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0493	3e-36	3329243	(AE001350) hypothetical protein [Chlamydia trachomatis]	3.1
1671	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	141103	HYPOTHETICAL PROTEIN ORF-1137 mouse	0.038
1672	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	198651	(M29325) ORF1 [Mus musculus]	0.006
1673	U49082	Human transporter protein (g17) mRNA, complete cds	3e-36	1840045	(U49082) transporter protein [Homo sapiens]	2e-15
1674	J03133	Human transcription factor SP1 mRNA, 3' end.	3e-36	477133	HF-1 regulatory element binding protein - rat	2e-31
1675	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	1e-36	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	4e-37
1676	M34857	Mouse Hox-2.5 mRNA.	9e-37	106296	homeotic protein Hox B9 - human (fragment)	0.15
1677	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	9e-37	2072960	(U93568) p40 [Homo sapiens]	3e-05
1678	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	8e-37	4185944	(Y17833) env protein [Human endogenous retrovirus K]	1e-15

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1679	Z93943	sequence from cosmid U235H3 on chromosome X	9e-38	106322	hypothetical protein (L1H 3' region) - human	4e-13
1680	X97303	H.sapiens mRNA for Ptg-12 protein	4e-38	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi\|630780\|pir\|\|S44909 ZK686.4 protein - Caenorhabditis elegans >gi\|304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]	3e-37
1681	Y08999	H.sapiens mRNA for Sop2p-like protein	3e-38	3334339	SOP2-LIKE PROTEIN	5e-06
1682	Z62887	H.sapiens CpG DNA, clone 74g6, forward read cpg74g6.ft1a .	2e-38	1245686	(U53181) F36D4.2 gene product [Caenorhabditis elegans]	0.19
1683	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	1e-38	59977	(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	1e-06
1684	D86974	Human mRNA for KIAA0220 gene, partial cds	1e-38	3337386	(AC002544) Unknown gene product splice form-2 [Homo sapiens]	8e-11
1685	M31013	Human nonmuscle myosin heavy chain (NMHC) mRNA, 3' end.	1e-38	4115748	(AB022023) nonmuscle myosin heavy chain B	2e-11
1686	AF006087	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds	4e-39	<NONE>	<NONE>	<NONE>
1687	X58374	D.melanogaster crn mRNA	4e-39	2655888	(AL009171) 62D9.a [Drosophila melanogaster]	4e-42
1688	D85815	Human DNA for rhoHP1, complete cds	1e-39	134080	GTP-BINDING PROTEIN TC10 ras-like protein [Homo sapiens]	3e-26

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1689	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	4e-40	1438534	(U49057) rA9 [Rattus norvegicus]	5e-05
1690	Y08999	H.sapiens mRNA for Sop2p-like protein	4e-40	3334339	SOP2-LIKE PROTEIN	9e-08
1691	AB002293	Human mRNA for KIAA0295 gene, partial cds	4e-40	2224531	(AB002293) KIAA0295 [Homo sapiens]	1e-30
1692	AF086222	Homo sapiens full length insert cDNA clone ZC66E08	1e-40	2829669	DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) >gi\|1707502\|gnl\|PID\|e254627 (X99227) double-stranded RNA-specific editase [Homo sapiens] editase 1 hRED1-L [Homo sapiens] >gi\|2039300 (U76421) dsRNA adenosine deaminase DRADA2b [Homo sapiens]	0.61
1693	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase (SCAD-SRL) mRNA, complete cds	1e-40	4105190	(AF044127) peroxisomal short-chain alcohol dehydrogenase	2e-06
1694	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi\|338088 (M74558) SIL	6e-23
1695	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi\|338088 (M74558) SIL	6e-23
1696	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi\|338088 (M74558) SIL	5e-23
1697	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi\|338088 (M74558) SIL	5e-23
1698	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-40	3882205	(AB018285) KIAA0742 protein [Homo sapiens]	6e-31

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ATP-BINDING CASSETTE	
1699	X75927	M.musculus abc2 mRNA	1e-40	728773	TRANSPORTER 1 ABC1 - human >gi\|495257 (X75926) abc1 [Mus musculus]	3e-37
1700	AF038200	Homo sapiens clone 23954 mRNA sequence	5e-41	3211975	(AF068195) putative glialblastoma cell differentiation-related protein [Homo sapiens]	5e-14
1701	U20521	Human estrogen sulfotransferase (STE) gene, exon 8 and complete cds	4e-41	<NONE>	<NONE>	<NONE>
1702	AF026548	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-41	3182923	[3-METHYL-2-OXOBUTANOATE DEHYDROGENASE (LIPOAMIDE)] KINASE PRECURSOR alpha-ketoacid dehydrogenase kinase precursor [Homo sapiens]	2e-09
1703	Y07660	M.tuberculosis accBC gene	2e-41	465847	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi\|280542\|pir\|\|S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST ...	3e-38
1704	AG001237	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	1e-41	106322	hypothetical protein (L1H 3' region) - human	5e-09
1705	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	1e-41	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	3e-12
1706	AF055029	Homo sapiens clone 24711 mRNA sequence	5e-42	3250681	(AL024486) putative protein	2.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					1-	
1707	Z49747	O.cuniculus mRNA for phospholipase C	5e-42	130227	PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) >gi\|163538 (M20638) phospholipase C-III [Bos taurus]	5e-36
1708	M93651	Human set gene, complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1709	AJ236940	Sus scrofa mRNA for hypothetical protein (5'; clone 7C4)	2e-42	2062403	(U79010) delta 6 desaturase [Borago officinalis]	8.5
1710	J03634	Human erythroid differentiation protein mRNA	2e-42	1708436	INHIBIN BETA A CHAIN PRECURSOR	2e-10
1711	AJ223777	Mus musculus mRNA for striatin	6e-43	2494917	STRIATIN >gi\|1495773\|gnl\|PID\|e254158	2e-32
1712	AF016411	Homo sapiens potassium channel subunit KCNA3.1B	2e-43	2708514	(AF016411) KCNA3.1B [Homo sapiens]	3e-13
1713	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	1e-43	111814	hypothetical protein 3 - rat >gi\|56589	2e-06
1714	X82895	H.sapiens mRNA for DLG2	6e-44	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS, LARGE HOMOLOG 2)	6e-52
1715	U17077	Human BENE mRNA, partial cds.	3e-44	53912	(X57960) ribosomal protein L7 [Mus musculus] >gi\|55489	8e-30
1716	AJ222700	Homo sapiens mRNA for TSC-22 protein	2e-44	<NONE>	<NONE>	<NONE>
1717	J03634	Human erythroid differentiation protein mRNA	2e-44	124279	INHIBIN BETA A CHAIN PRECURSOR PROTEIN) (EDF) >gi\|87936\|pir\|\|B24248 inhibin beta-A chain precursor - human >gi\|181947 (J03634) erythroid differentiation protein precursor [Homo sapiens] sapiens] >gi\|226850\|prf\|\|1608260B inhibin betaA [Homo sapiens]	0.73

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1718	AB014518	Homo sapiens mRNA for KIAA0618 protein, complete cds	7e-45	1911548	(S80864) cytochrome c-like polypeptide sapiens]	1.6
1719	X76808	H.sapiens genomic DNA clone d2	7e-45	868201	(U29380) similar to adenylate cyclase [Caenorhabditis elegans]	2e-09
1720	AB021288	Homo sapiens mRNA for beta 2-microglobulin, complete cds	2e-45	2465521	(U95995) RNA-dependent RNA polymerase [Cryptosporidium parvum]	0.15
1721	X63468	H.sapiens mRNA for transcription factor TFIIE alpha	8e-46	<NONE>	<NONE>	<NONE>
1722	AF019226	Homo sapiens D2-2 mRNA, 3'UTR	7e-46	<NONE>	<NONE>	<NONE>
1723	D31764	Human mRNA for KIAA0064 gene, complete cds	2e-46	3123050	HYPOTHETICAL PROTEIN KIAA0064	1e-15
1724	K02774	Human MHC class II HLA-DR-beta-psi (DW4/DR4) pseudogene, exons 3,4, 5,6, clones cosII-3301 and cosII-801.	1e-46	4185946	(Y17834) gag protein [Human endogenous retrovirus K]	2e-14
1725	X92109	H.sapiens hcgIX gene	9e-47	2498185	BRIDE OF SEVENLESS PROTEIN PRECURSOR >gi\|1079166\|pir\|\|A47550 bride of sevenless precursor - fruit fly (Drosophila virilis) >gi\|290216 virilis]	1.4
1726	X93334	H.sapiens mitochondrial DNA, complete genome	8e-47	128753	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi\|86696\|pir\|\|A00435 NADH dehydrogenase (ubiquinone)	4e-15
1727	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-47	<NONE>	<NONE>	<NONE>
1728	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	3e-47	4185944	(Y17833) env protein [Human endogenous retrovirus K]	7e-18
1729	Z63594	H.sapiens CpG DNA, clone 87f9, forward read cpg87f9.ft1a .	1e-47	3322743	(AE001222) T. pallidum predicted coding region TP0454	2.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1730	X62295	R.rattus mRNA for vascular type-1 angiotensin II receptor	4e-48	1209756	(U43629) integral membrane protein [Beta vulgaris]	1e-07
1731	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-48	<NONE>	<NONE>	<NONE>
1732	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	4e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1733	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	3e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1734	X62295	R.rattus mRNA for vascular type-1 angiotensin II receptor	1e-49	1209756	(U43629) integral membrane protein [Beta vulgaris]	7e-12
1735	AJ007509	Homo sapiens mRNA for E1B-55kDa-associated protein	1e-49	3319956	(AJ007509) E1B-55kDa-associated protein	4e-24
1736	X97303	H.sapiens mRNA for Ptg-12 protein	1e-49	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi\|630780\|pir\|\|S44909 ZK686.4 protein - Caenorhabditis elegans >gi\|304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]	8e-39
1737	AF038404	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds	4e-50	<NONE>	<NONE>	<NONE
1738	L43618	Homo sapiens polycystic kidney disease (PKD1) gene, exons 35-42	4e-50	903758	(L43619) polycystic kidney disease 1 protein [Homo sapiens]	3e-0
1739	AF009424	Homo sapiens clone 22 mRNA, alternative splice variant alpha-1, complete cds	4e-50	2271473	(AF009426) clone 22 [Homo sapiens]	5e-

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1740	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence.	2e-50	99758	monosaccharid transport protein STP4 - Arabidopsis thaliana >gi\|16524 (X66857) sugar transport protein [Arabidopsis thaliana]	6.4
1741	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	2e-50	2072960	(U93568) p40 [Homo sapiens]	2e-05
1742	U80745	Homo sapiens CTG7a mRNA, partial cds	1e-50	<NONE>	<NONE>	<NONE>
1743	D84514	Bovine mRNA for p97, partial cds	1e-50	3978527	(AF103728) structural polyprotein [Sindbis virus]	9.9
1744	M22960	Human protective protein mRNA, complete cds.	1e-50	131081	LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR (CATHEPSIN A) (CARBOXYPEPTIDASE C) human >gi\|190283 (M22960) protective protein precursor	1e-12
1745	X86018	H.sapiens mRNA for MUF1 protein	1e-50	1082610	muf1 protein - human >gi\|762953 (X86018) muf1 [Homo sapiens]	1e-21
1746	U03495	Human transcription factor LSF-ID mRNA, complete cds.	7e-51	2136296	transcription factor LSF - human >gi\|476099	1e-21
1747	AB015344	Homo sapiens HRIHFB2157 mRNA, partial cds	5e-51	3970874	(AB015344) HRIHFB2157 [Homo sapiens]	2e-35
1748	M93339	Human zinc finger protein mRNA.	4e-51	3024110	MYC-ASSOCIATED ZINC FINGER PROTEIN sapiens]	2e-06
1749	U71363	Human zinc finger protein zfp6 (ZF6) mRNA, partial cds	4e-51	2689441	(AC003682) F18547_1 [Homo sapiens]	2e-11
1750	X56932	H.sapiens mRNA for 23 kD highly basic protein	4e-51	730451	60S RIBOSOMAL PROTEIN L13A (23 KD HIGHLY BASIC PROTEIN) >gi\|345897\|pir\|\|S29539 basic protein, 23K - human >gi\|23691 (X56932) 23 kD highly basic protein [Homo sapiens]	1e-11
1751	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA21E11	2e-51	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1752	AF068245	BAF60b gene, partial sequence	5e-52	<NONE>	<NONE>	<NONE>
1753	AJ236932	Sus scrofa mRNA for hypothetical protein (5'; clone 4B8)	5e-52	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1754	AF003693	Mus musculus scaffold protein Pbp1 homolog mRNA, complete cds	6e-53	2197106	(AF003693) scaffold protein Pbp1 homolog [Mus musculus]	2e-54
1755	M27319	Human calmodulin mRNA, complete cds.	5e-53	115528	CALMODULIN >gi\|102408\|pir\|\|JC1309 calmodulin - Stylonychia lemnae (SGC5) >gi\|161195	0.002
1756	M74555	Mouse house-keeping protein mRNA, complete cds.	5e-53	284775	house-keeping protein - mouse >gi\|193871	5e-30
1757	X92720	H.sapiens mRNA for phosphoenolpyruvate carboxykinase	6e-54	2135915	phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32) precursor, mitochondrial - human carboxykinase (GTP) [Homo sapiens]	6e-21
1758	AF007872	Homo sapiens torsinB (DQ1) mRNA, partial cds	2e-54	2760121	(AB002405) LAK-4p [Homo sapiens]	0.27
1759	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds.	2e-54	1236083	(U49507) Lisch7 [Mus musculus]	3e-27
1760	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	1e-55	2370371	(Y14657) hydrophobin [Pleurotus ostreatus] >gi\|2982620\|gnl\|PID\|e1283986 (AJ225061) POH2 hydrophobin [Pleurotus ostreatus]	2.0
1761	U83702	Human cytochrome c oxidase subunit VIa gene, exon 3 and complete cds	8e-56	2982994	(AE000682) hypothetical protein [Aquifex aeolicus]	7.0
1762	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	7e-56	3021409	(Y12781) transducin (beta) like 1 protein [Homo sapiens]	7e-39

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1763	AB020673	Homo sapiens mRNA for KIAA0866 protein, complete cds	8e-57	2104553	(AF001548) Myosin heavy chain (MHY11) (5'partial) [Homo sapiens]	4e-04
1764	AJ236932	Sus scrofa mRNA for hypothetical protein (5'; clone 4B8)	3e-57	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1765	L06900	Human dystrophin gene, intron 1 containing pseudo exon.	1e-58	4185129	(AC005724) unknown protein [Arabidopsis thaliana] thaliana]	7.0
1766	X93334	H.sapiens mitochondrial DNA, complete genome	9e-59	1492050	(U60315) MC107L [Molluscum contagiosum virus subtype 1]	0.17
1767	AF064856	Rattus sp. 7acomp protein mRNA, complete cds	3e-59	3169626	(AF064856) 7acomp protein [Rattus sp.]	2e-31
1768	AF081484	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds	2e-59	32015	(X06956) alpha-tubulin [Homo sapiens]	4e-22
1769	X71427	Homo sapiens mRNA for FUS-CHOP protein fusion	1e-60	746557	(U23523) histidine-rich [Caenorhabditis elegans]	0.45
1770	AF013988	Homo sapiens serine protease mRNA, complete cds	1e-60	2564316	(AB006622) No similarities to any reported proteins [Homo sapiens]	0.26
1771	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	7e-61	2137490	lymphocyte specific helicase - mouse musculus]	3e-25
1772	X93334	H.sapiens mitochondrial DNA, complete genome	4e-61	70656	ubiquitin / ribosomal protein S27a - human extension protein, HUBCEP80 [human, Peptide, 156 aa] ubiquitin extention protein [Cavia porcellus]	9e-08
1773	D38255	Homo sapiens mRNA for CAB1, complete cds	4e-61	2135214	gene MLN 64 protein - human	4e-23
1774	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	8e-62	2137490	lymphocyte specific helicase - mouse musculus]	8e-26

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1775	M21731	Human lipocortin-V mRNA, complete cds.	6e-62	3212603	Human Annexin V With Proline Substitution By Thioproline	2e-20
1776	AF021936	Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta (MRCK-beta) mRNA, complete cds	2e-62	2736153	(AF021936) myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta [Rattus norvegicus]	3e-27
1777	Y12059	H.sapiens HUNKI mRNA	1e-62	3184498	(AC004798) R31546_1 [Homo sapiens]	3e-09
1778	L37368	Human (clone E5.1) RNA-binding protein mRNA, complete cds.	6e-63	477578	sialidase - Actinomyces viscosus >gi\|141852	7.8
1779	M27877	Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.	5e-63	1731443	ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) >gi\|106023\|pir\|\|A32891 finger protein 1, placental - human	3e-33
1780	AF095448	Homo sapiens putative G protein-coupled receptor	2e-63	3116131	(AL023288) hypothetical protein	4.6
1781	L19437	Human transaldolase mRNA containing transposable element, complete cds	2e-63	1553119	(U63159) transaldolase [Mus musculus]	4e-18
1782	L41351	Homo sapiens prostasin mRNA, complete cds	1e-63	2833277	PROSTASIN PRECURSOR precursor - human >gi\|862305 (L41351) prostasin [Homo sapiens] >gi\|1143194 (U33446) prostasin [Homo sapiens]	6e-14
1783	AF053470	Homo sapiens 10kD protein (BC10) mRNA, complete cds	6e-64	482237	hypothetical protein K03H1.9 - Caenorhabditis elegans	0.029

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1784	D37791	Mouse mRNA for beta-1,4-galactosyltransferase	6e-64	3880102	(Z93390) similar to FYVE zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans] zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans]	3e-16
1785	AF015770	Mus musculus radical fringe (radical-fringe) mRNA, complete cds	6e-64	2204355	(U94350) radical fringe precursor [Mus musculus]	1e-36
1786	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA21E11	2e-64	<NONE>	<NONE>	<NONE>
1787	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	1e-64	2447063	(U42580) A565R [Paramecium bursaria Chlorella virus 1]	8.8
1788	Y10211	H.sapiens LAG-3 gene, promoter region	7e-65	1944540	(X14112) tegument protein [human herpesvirus 1]	2.3
1789	M19045	Human lysozyme mRNA, complete cds.	2e-65	<NONE>	<NONE>	<NONE>
1790	U01882	Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds	2e-65	585401	LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN) >gi\|480045\|pir\|\|S36249 lipB protein - Pseudomonas glumae >gi\|49207 (X70354) helper protein	4.2
1791	AF069517	Homo sapiens RNA binding protein DEF-3 mRNA, complete cds	2e-65	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	1e-25

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens jerky				
1792	AF004715	gene product homolog mRNA, complete cds	2e-65	2314829	(AF004715) jerky gene product homolog [Homo sapiens]	2e-45
1793	X59652	C. longicaudatus hprt mRNA for hypoxanthine	3e-66	631625	hypoxanthine (guanine) phosphoribosyltransferase - long-tailed hamster phosphoribosyltransferase [Cricetulus longicaudatus]	6e-54
1794	U94350	Mus musculus radical fringe precursor mRNA, complete cds	3e-67	2204355	(U94350) radical fringe precursor [Mus musculus]	2e-33
1795	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	3e-68	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	7e-51
1796	J03137	Cow phosphoinositide-specific phospholipase C	3e-69	226908	phospholipase C 154 [Bos taurus]	3e-25
1797	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	1e-69	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	2e-33
1798	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	4e-70	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	3e-19
1799	X65157	M.musculus mRNA for desmoyokin, partial	5e-74	109781	desmoyokin - mouse (fragment) >gi\|50675	9e-37
1800	Z97207	Mus musculus mRNA for B-IND1 protein	2e-74	2231019	(Z97207) B-IND1 protein [Mus musculus]	6e-21
1801	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds.	6e-75	984814	(U27196) zinc finger protein [Gallus gallus] gallus]	2e-44

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					70 KD WD-REPEAT TUMOR-	
1802	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-77	3123027	SPECIFIC ANTIGEN >gi\|2505957\|gnl\|PID\|e353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	4e-42
1803	X65157	M.musculus mRNA for desmoyokin, partial	3e-79	109781	desmoyokin - mouse (fragment) >gi\|50675	9e-33
1804	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	2e-84	1362781	cytokine inducible nuclear protein C193 - human >gi\|793841 (X83703) nuclear protein [Homo sapiens]	7e-30
1805	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-84	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	6e-43
1806	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	6e-85	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-41
1807	U19181	Rattus norvegicus Rabin3 mRNA, complete cds.	2e-87	624225	(U19181) Rabin3 [Rattus norvegicus]	2e-41
1808	U40342	Mus musculus ninein mRNA, complete cds.	1e-91	1113865	(U40342) ninein [Mus musculus]	2e-36
1809	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	4e-92	136077	TROPOMYOSIN BETA 3, FIBROBLAST chicken >gi\|515694 (M23082) tropomyosin [Gallus gallus]	0.56
1810	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	5e-93	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-50
1811	AF035527	Mus musculus EHF (Ehf) mRNA, complete cds	2e-95	3138930	(AF035527) EHF [Mus musculus]	2e-47

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1812	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	6e-96	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	7e-41
1813	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	7e-97	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	3e-41
1814	X90849	G.gallus PB1 gene	2e-97	2134381	polybromo 1 protein - chicken chicken >gi\|951231 (X90849) polybromo 1 protein [Gallus gallus]	1e-34
1815	S79873	h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	3e-98	<NONE>	<NONE>	<NONE>
1816	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	2e-98	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	9e-39
1817	L14684	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	e-100	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi\|543383\|pir\|\|S40780 translation elongation factor G, mitochondrial - rat >gi\|310102	2e-30
1818	X84692	M.musculus Spnr mRNA for RNA binding protein	e-133	1363238	spermatid perinuclear RNA-binding protein Spnr - mouse >gi\|673454 (X84692) spermatid perinuclear RNA binding protein [Mus musculus]	5e-35
1819	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	e-113	1362781	cytokine inducible nuclear protein C193 - human >gi\|793841 (X83703) nuclear protein [Homo sapiens]	2e-36
1820	S66855	HoxB9=Hox-2.5 [mice, embryos, mRNA Partial, 786 nt]	e-107	1708355	HOMEOBOX PROTEIN HOX-B9 (HOX-2.5)	8e-37

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HoxB9=Hox-2.5				
1821	S66855	[mice, embryos, mRNA Partial, 786 nt]	e-108	1708355	HOMEOBOX PROTEIN HOX-B9 (HOX-2.5)	4e-37
1822	U92072	Rattus norvegicus m-tomosyn mRNA, complete cds	e-102	3790389	(U92072) m-tomosyn [Rattus norvegicus]	2e-38
1823	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-129	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi\|407339\|gnl\|PID\|d1005029 (D17577) Kif1b [Mus musculus]	2e-39
1824	AF062484	Mus musculus SDP8 mRNA, complete cds	e-122	3126981	(AF062484) SDP8 [Mus musculus]	5e-40
1825	X73683	R.norvegicus mRNA for histone H3.3	e-109	122075	(H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi\|2119023\|pir\|\|S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136) [Oryctolagus cuniculus] >gi\|8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi\|51198 gallus] >gi\|161190 (M17876) histone H3 [Spisula solidissima] >gi\|211853 (M11393) histone 3.3 [Gallus gallus] >gi\|306848 (M11354) H3.3 histone [Homo sapiens] melanogaster] >gi\|963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	2e-40
1826	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	e-102	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	2e-40
1827	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-131	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi\|407339\|gnl\|PID\|d1005029 (D17577) Kif1b [Mus musculus]	7e-42

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1828	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-131	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	3e-43
1829	U09874	Mus musculus SKD3 mRNA, complete cds.	e-122	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	7e-48
1830	X99145	C.familiaris mRNA for C3VS protein	e-110	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [Canis familiaris]	2e-49
1831	X99836	P.walti mRNA for rnp associated protein 55	e-106	4200286	(X99836) rap55 [Pleurodeles waltl]	2e-50
1832	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	e-121	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	3e-51
1833	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	e-118	3372657	(AF060246) zinc finger protein 106 [Mus musculus]	1e-52
1834	Z14030	R.norvegicus mRNA for TRAP-complex gamma subunit.	e-120	1174453	TRANSLOCON-ASSOCIATED PROTEIN, GAMMA SUBUNIT (TRAP-GAMMA) (SIGNAL SEQUENCE RECEPTOR GAMMA SUBUNIT) (SSR-GAMMA) >gi\|423185\|pir\|\|S33294 translocon-associated protein gamma chain - rat norvegicus]	7e-54
1835	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	e-132	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	5e-54
1836	L20427	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-116	457372	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [Rattus norvegicus]	4e-56

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROTEIN TSG24 (MEIOTIC	
1837	X80169	M.musculus mRNA for 200 kD protein	e-122	1717793	CHECK POINT REGULATOR) >gi\|1083553\|pir\|\|A55117 tsg24	2e-56
1838	AF080568	Rattus norvegicus CTP:phosphoethanolamine cytidylyltransferase mRNA, complete cds	e-119	3396102	(AF080568) CTP:phosphoethanolamine cytidylyltransferase	6e-58
1839	X99145	C.familiaris mRNA for C3VS protein	e-121	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [Canis familiaris]	2e-58
1840	AF019075	Pan troglodytes breast and ovarian cancer susceptibility (BRCA1) gene, partial cds	e-145	2218154	(AF005068) breast and ovarian cancer susceptibility protein splice variant [Homo sapiens]	1e-58
1841	U55042	Bos taurus myosin X, complete cds	e-122	1755049	(U55042) myosin X [Bos taurus]	1e-61
1842	AJ007780	Mus musculus mRNA for poly(ADP-ribose) polymerase-2	e-119	3283975	(AF072521) poly-(ADPribosyl)-transferase homolog PARP	4e-62
1843	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	e-105	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	3e-62
1844	U55042	Bos taurus myosin X, complete cds	e-121	1755049	(U55042) myosin X [Bos taurus]	1e-62
1845	X61506	Mouse E46 mRNA for E46 protein	e-139	114909	BRAIN PROTEIN E46	9e-67
1846	D90335	Bovine mRNA for GTP-binding protein alpha-subunit	e-148	585174	GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-14 SUBUNIT (GL1) >gi\|108711\|pir\|\|A40891 GTP-binding protein GL1 alpha chain - bovine protein, alpha-subunit [Bos taurus]	2e-69
1847	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds.	e-140	2121326	(AC002128) Lisch7 [Homo sapiens]	2e-74

PP01598 / 200130.512
Table 4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
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3	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
6	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
7	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
8	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
9	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
10	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
11	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
12	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
13	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
14	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
15	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
16	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
17	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
18	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
19	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
20	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
21	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
22	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
23	<NONE>	<NONE>	<NONE>	1079469	tMDC I protein - crab-eating macaque	9.3
24	<NONE>	<NONE>	<NONE>	3043656	(AB011138) KIAA0566 protein [Homo sapiens]	9.3
25	<NONE>	<NONE>	<NONE>	112175	potassium channel protein RK5 - rat protein [Rattus norvegicus]	8.6
26	<NONE>	<NONE>	<NONE>	3769624	(AF091565) olfactory receptor [Rattus norvegicus]	7.2
27	<NONE>	<NONE>	<NONE>	3876443	(Z81517) F28B1.6 [Caenorhabditis elegans]	7.1
28	<NONE>	<NONE>	<NONE>	2224464	(AB001684) ORF249 [Chlorella vulgaris]	6.9
29	<NONE>	<NONE>	<NONE>	1519707	(U67940) ORFveg106; random cDNA sequence [Dictyostelium discoideum]	6.7
30	<NONE>	<NONE>	<NONE>	227491	protein kinase C II [Xenopus laevis]	6.7
31	<NONE>	<NONE>	<NONE>	630575	C50C3.4 protein - Caenorhabditis elegans	6.0
32	<NONE>	<NONE>	<NONE>	137290	35 KD PROTEIN IN RNA2 clover necrotic mosaic virus >gi\|61466 (X08021) ORF for 35 kDa polypeptide (AA 1-317) [Red clover necrotic mosaic virus]	6.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(X16711) pid:g30041 [Homo	
33	<NONE>	<NONE>	<NONE>	30041	sapiens]	5.9
34	<NONE>	<NONE>	<NONE>	2493585	CELL DIVISION PROTEIN FTSW	5.7
35	<NONE>	<NONE>	<NONE>	1001450	(D63999) hypothetical protein	5.7
36	<NONE>	<NONE>	<NONE>	3182918	NITROGEN REGULATORY PROTEIN AREA	5.2
37	<NONE>	<NONE>	<NONE>	140011	MITOCHONDRIAL RIBOSOMAL PROTEIN S5 Emericella nidulans mitochondrion (SGC3) >gi\|12709 nidulans] >gi\|472822 (J01390) unknown protein	4.3
38	<NONE>	<NONE>	<NONE>	3979943	(AL034393) predicted using Genefinder; similar to WD domain, G-beta repeat; cDNA EST yk362f7.5 comes from this gene; cDNA EST yk362f7.3 comes from this gene [Caenorhabditis elegans]	4.0
39	<NONE>	<NONE>	<NONE>	950203	(U31329) polyketide synthase [Aspergillus terreus]	3.3
40	<NONE>	<NONE>	<NONE>	3560232	(AL031530) hypothetical zinc finger protein [Schizosaccharomyces pombe]	3.0
41	<NONE>	<NONE>	<NONE>	730071	AXONEME-ASSOCIATED PROTEIN MST101(1) product [Drosophila hydei]	2.6
42	<NONE>	<NONE>	<NONE>	2506641	HYPOTHETICAL 21.7 KD PROTEIN IN INTE-PIN INTERGENIC REGION >gi\|1787402 (AE000214) orf, hypothetical protein [Escherichia coli]	2.5
43	<NONE>	<NONE>	<NONE>	3511232	(AF071556) anthranilate dioxygenase large subunit	2.4
44	<NONE>	<NONE>	<NONE>	1150900	(U43139) envelope glycoprotein gp120 [Human immunodeficiency virus type 1]	1.9
45	<NONE>	<NONE>	<NONE>	3876099	(Z75536) similar to dynein heavy chain; cDNA EST EMBL:D27549 comes from this gene; cDNA EST EMBL:D34859 comes from this gene [Caenorhabditis elegans]	1.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AL032647) predicted using	
46	<NONE>	<NONE>	<NONE>	3881150	Genefinder	1.4
47	<NONE>	<NONE>	<NONE>	132200	COLANIC ACID CAPSULAR BIOSYNTHESIS ACTIVATION PROTEIN A >gi\|95605\|pir\|\|S17701 rcsA protein	1.1
48	<NONE>	<NONE>	<NONE>	2204286	(U61380) germination protein [Bacillus megaterium]	1.0
49	<NONE>	<NONE>	<NONE>	1723955	HYPOTHETICAL 11.4 KD PROTEIN IN FOX1-KEX1 INTERGENIC REGION >gi\|2132566\|pir\|\|S64222 probable membrane protein YGL204c - yeast (Saccharomyces cerevisiae) >gi\|1322838\|gnl\|PID\|e243803 (Z72726) ORF YGL204c [Saccharomyces cerevisiae]	0.84
50	<NONE>	<NONE>	<NONE>	3201564	(AJ006514) prolipoprotein diacylglyceryl transferase [Vibrio cholerae]	0.31
51	<NONE>	<NONE>	<NONE>	2808721	(AL021428) hypothetical protein Rv0064	0.27
52	<NONE>	<NONE>	<NONE>	602434	(U17986) GABA/noradrenaline transporter [Homo sapiens]	0.13
53	<NONE>	<NONE>	<NONE>	3347955	(AF076184) cytosolic sorting protein PACS-1b [Rattus norvegicus]	0.12
54	<NONE>	<NONE>	<NONE>	1255887	(U53344) coded for by C. elegans cDNA yk92b4.5; coded for by C. elegans cDNA yk73a1.5; coded for by C. elegans cDNA yk102e9.5; coded for by C. elegans cDNA yk71c8.5; coded for by C. elegans cDNA yk66d11.5; coded for by C. elegans cDNA yk66c3...	0.074
55	<NONE>	<NONE>	<NONE>	103076	Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster)	0.003
56	<NONE>	<NONE>	<NONE>	107560	Ras inhibitor (clone JC265) - human sapiens]	0.002

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					Bkm-like sex-determining	
57	<NONE>	<NONE>	<NONE>	103076	region hypothetical protein CS314 - fruit fly (Drosophila melanogaster)	2e-04
58	<NONE>	<NONE>	<NONE>	2702370	(AF038604) contains similarity to Drosophila ovarian tumor locus protein (GB:X13693) [Caenorhabditis elegans]	6e-05
59	<NONE>	<NONE>	<NONE>	3859713	(AL033501) phox domain protein [Candida albicans]	3e-05
60	<NONE>	<NONE>	<NONE>	2088839	(AF003386) F59E12.5 gene product [Caenorhabditis elegans]	2e-08
61	<NONE>	<NONE>	<NONE>	121059	GC-RICH SEQUENCE DNA-BINDING FACTOR GCF - human >gi\|179412 (M29204) DNA-binding factor [Homo sapiens]	4e-09
62	<NONE>	<NONE>	<NONE>	3875246	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...	9e-24
63	<NONE>	<NONE>	<NONE>	1465834	(U64857) No definition line found [Caenorhabditis elegans]	9e-28
64	<NONE>	<NONE>	<NONE>	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-29
65	<NONE>	<NONE>	<NONE>	3880433	(Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	8e-31
66	D42133	Rat annexin V gene, exon7 and exon8	5.0	<NONE>	<NONE>	<NONE>
67	L35679	Homo sapiens (subclone H8 2_d11 from P1 35 H5 C8) DNA sequence.	5.0	1086902	(U41278) coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [Caenorhabditis elegans]	6.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 strain BX220				
68	U90184	from USA, envelope glycoprotein C2V3 region (env) gene, partial cds	5.0	1297070	(Z71986) convicilin precursor [Vicia narbonensis]	6.6
69	U61465	Human myosin VIIa (MYO7A) gene, 5' exon 37	5.0	2313225	(AE000535) L-lactate permease (lctP) [Helicobacter pylori 26695]	5.0
70	AF013717	Homo sapiens periplakin (PPL) mRNA, partial cds	5.0	3719238	(AF064869) brain-enriched guanylate kinase-associated protein 2; BEGA2 [Rattus norvegicus]	3.8
71	X58245	Soybean mRNA for HMG-1 like protein	5.0	2995363	(AL022245) biotin synthase	0.99
72	AF102425	Frasera paniculata tRNA-Leu (trnL) gene, intron, chloroplast sequence	4.9	3522958	(AC004411) putative pectinesterase [Arabidopsis thaliana]	6.4
73	X82817	H.sapiens PTP1C/HCP-variant gene	4.9	3875514	(Z81494) cDNA EST EMBL:D27474 comes from this gene; cDNA EST EMBL:D27473 comes from this gene; cDNA EST EMBL:T00471 comes from this gene; cDNA EST EMBL:D34192 comes from this gene; cDNA EST EMBL:D37241 comes from this gene; ...	2.8
74	U04827	Mus musculus brain fatty acid-binding protein	4.9	3676132	(AL031765) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=31.96; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SPTREMBL:Q93319; 2-match_description=HYPOTHETICAL PROTEIN C33A11.2.;...	2e-09
75	AF038859	Neospora hughesi strain NE1 internal transcribed spacer 1, complete sequence	4.8	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		M.musculus MFH-1				
76	Y08222	gene	4.8	<NONE>	<NONE>	<NONE>
77	AJ224475	Borrelia burgdorferi left chromosomal subtelomeric region (pfpB gene)	4.8	4218141	(AJ236702) HMR1 protein [Antirrhinum majus]	8.3
78	U02486	Mus musculus LAF putative membrane protein (KRAG) gene, exon 3 and complete cds	4.8	3258103	(AP000006) 367aa long hypothetical protein [Pyrococcus horikoshii]	2.7
79	AB000280	Rat mRNA for peptide/histidine transporter, complete cds	4.8	806317	(M29067) unknown protein [Saccharomyces cerevisiae]	0.001
80	Z49771	A.cepa mitochondrial gene for NADH dehydrogenase subunit 3 and ribosomal protein S12	4.5	<NONE>	<NONE>	<NONE>
81	M63494	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 6 and 7, clones lambda-Fc(3.2,93).	4.3	<NONE>	<NONE>	<NONE>
82	Z14035	S.pombe car1 gene	2.0	3790665	(AF099000) No definition line found [Caenorhabditis elegans]	1.2
83	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes	2.0	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi\|2832633\|gnl\|PID\|e1249651 (AL021711) putative protein [Arabidopsis thaliana]	2e-26
84	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	2.0	4176500	(AL031177) dJ889M15.3 (novel protein)	9e-59
85	U79292	Human clone 23734 mRNA sequence	1.9	<NONE>	<NONE>	<NONE>
86	V00159	Chloroplast Euglena gracilis gene coding for the 5S and 16S rRNA.	1.9	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis XL-				
87	U95094	INCENP (XL-INCENP) mRNA, complete cds	1.9	<NONE>	<NONE>	<NONE>
88	X93206	H.salinarium TATA box-binding protein genes and ORFs	1.9	<NONE>	<NONE>	<NONE>
89	U60979	Caenorhabditis elegans programmed cell death specifier (ces-2) gene, complete cds	1.9	<NONE>	<NONE>	<NONE>
90	X56272	C. tentans ORF's (A-E) for hemoglobin	1.9	<NONE>	<NONE>	<NONE>
91	L22383	Homo sapiens DNA sequence, repeat region.	1.9	<NONE>	<NONE>	<NONE>
92	U82814	Hirudo medicinalis neuron-specific protein mRNA, complete cds	1.9	3822533	(AF094531) immunoglobulin heavy chain precursor	2.0
93	U18504	Haplomitrium hookeri 18S rRNA gene, partial sequence.	1.9	1083969	hypothetical protein 6 - fowlpox virus virus]	2.0
94	X53676	Pseudomonas stutzeri nosDFY genes involved in copper processing	1.9	2980781	(AL022198) putative protein	0.70
95	U60086	Dictyostelium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds.	1.9	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	6e-05
96	U33447	Human putative G-protein-coupled receptor (GPR17) gene, complete cds	1.9	3880034	(Z75550) similar to cell division control protein [Caenorhabditis elegans]	7e-14
97	M81327	Sus scrofa lactoferrin mRNA, complete cds. > :: gb\|I28421\|I28421 Sequence 5 from patent US 5571691	1.8	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		S.iniae lctP & lctO				
98	Y07622	genes and ORF1	1.8	<NONE>	<NONE>	<NONE>
99	M60474	Mouse myristoylated alanine-rich C-kinase substrate (MARCKS) mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
100	Y13901	Homo sapiens FGFR-4 gene	1.8	<NONE>	<NONE>	<NONE>
101	U44400	Human Down Syndrome region of chromosome 21, clone A31D6-1D6.	1.8	<NONE>	<NONE>	<NONE>
102	U92808	Ruminococcus albus beta-glucosidase (gluA) mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
103	L25051	Candida albicans argininosuccinate lyase (ARG4) gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
104	AE000546	Helicobacter pylori 26695 section 24 of 134 of the complete genome	1.8	<NONE>	<NONE>	<NONE>
105	J00978	Xenopus laevis major beta-globin gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
106	U41716	Human immunodeficiency virus type 1 isolate JW95-5, vpr gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
107	X66286	G.gallus mRNA for tensin	1.8	<NONE>	<NONE>	<NONE>
108	U76636	Xenopus calbindin D28k mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
109	J00664	rabbit embryonic beta-4-globin gene.	1.8	<NONE>	<NONE>	<NONE>
110	M21535	Human erg protein (ets-related gene) mRNA, complete cds.	1.8	2983160	(AE000693) hypothetical protein [Aquifex aeolicus]	7.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rat troponin T			(Z46595) incomplete interleukin-	
111	M80829	cardiac isoform gene, complete cds	1.8	999450	11 receptor isoform [Homo sapiens]	7.3
112	D37887	Cyprinus carpio c-myc gene for c-Myc, complete cds	1.8	3023408	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN (BRANCHED-CHAIN AMINO ACID UPTAKE CARRIER) >gi\|1075007\|pir\|\|D64056 membrane-associated component, branched amino acid transport system (brnQ) homolog - Haemophilus influenzae (strain Rd KW20) system II carrier protein (brnQ) [Haemophilus influenzae Rd]	7.2
113	AF019765	Homo sapiens G protein-coupled receptor kinase 1 and G protein-coupled receptor kinase 1b (GRK1) gene, alternatively spliced, alternative exon 6, exon 7, and partial cds	1.8	498643	(U10270) G-box binding factor 1 [Zea mays]	7.2
114	AF025967	Helicobacter pylori J166 virulence regulon transcriptional activator homolog gene, partial cds, strain-specific genomic sequence B2	1.8	3850108	(AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]	5.7
115	U13183	Xenopus laevis (Xwnt-4) mRNA, complete cds.	1.8	2494853	PROBABLE HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II) protein [Escherichia coli] >gi\|1786406 (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli]	5.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
116	S68944	Na+/Cl(-)-dependent neurotransmitter transporter	1.8	2276316	(Z96810) GLYT-1 LIKE [Homo sapiens]	5.5
117	M92905	Rat calcium channel alpha-1 subunit (rbB-I) mRNA, complete cds.	1.8	3165522	(AF067607) Similar to cuticular collagen; C18H7.3	5.5
118	X12429	Xenopus laevis U1 70K gene exon 10	1.8	2735957	(AF015685) reverse transcriptase domain protein	3.3
119	D83333	Mouse hepatitis virus genomic RNA for spike protein, partial cds	1.8	3876559	(Z81072) Similarity to Human cyclin A/CDK2-associatd protein P19 (RNA polymerase elongation factor) (SW:SKP1_HUMAN); cDNA EST EMBL:T00114 comes from this gene; cDNA EST yk390f11.5 comes from this gene; cDNA EST yk402e11.5 co... >gi\|3877216\|gnl\|PID\|e1346850 protein P19 (RNA polymerase elongation factor) gene; cDNA EST yk390f11.5 comes from this gene; cDNA EST yk402e11.5 co...	3.3
120	AF016972	Cervus elaphus REDDEER mitochondrial D-loop, complete sequence	1.8	3878057	(Z99942) similar to von Willebrand factor type A domain; cDNA EST yk412d4.5 comes from this gene; cDNA EST yk412d4.3 comes from this gene	3.2
121	AB010741	Oncorhynchus mykiss mRNA for rtSox24, complete cds	1.8	1730805	HYPOTHETICAL 21.0 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION >gi\|2132762\|pir\|\|S63129 probable membrane protein YNL174w - yeast (Saccharomyces cerevisiae) >gi\|1302152\|gnl\|PID\|e239548 (Z71451) ORF YNL174w [Saccharomyces cerevisiae]	2.5
122	U32844	Haemophilus influenzae Rd section 159 of 163 of the complete genome	1.8	728910	A-TYPE INCLUSION PROTEIN (ATI) camelpox virus >gi\|62381 (X69774) 84kDa A-type inclusion protein [unidentified]	1.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
123	U18321	Human ionizing radiation resistance conferring protein mRNA, complete cds.	1.8	2133273	ribosomal protein YS7 homolog Emericella nidulans	1.4
124	M28668	Human cystic fibrosis mRNA, encoding a presumed transmembrane conductance regulator (CFTR). > :: gb\|I11500\|I11500 Sequence 1 from Patent US 5407796	1.8	90492	filaggrin precursor - mouse (fragment)	0.87
125	AF064553	Mus musculus NSD1 protein mRNA, complete cds	1.8	2501207	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi\|1065461 (U40411) Similar to protein disulfide-isomerase. [Caenorhabditis elegans]	0.87
126	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.8	115131	REGULATORY PROTEIN BRLA (BRISTLE A PROTEIN) >gi\|83718\|pir\|\|A28913 regulatory protein brlA - Emericella nidulans >gi\|168029 (M20631) brlA protein	0.84
127	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1.8	2135624	metalloproteinase 1 (EC 3.4.24.-) - human	0.65
128	M37278	R.norvegicus renin gene, exons 1-9.	1.8	4050087	(AF109907) S164 [Homo sapiens]	0.58
129	X82879	Artificial sequences DNA for ART 2 consensus	1.8	310929	(L13442) cysteine-rich extensin-like protein-4 [Nicotiana tabacum]	0.52
130	D89729	Homo sapiens mRNA for CRM1 protein, complete cds	1.8	3559944	(AJ010792) Muc5AC protein [Mus musculus]	0.38
131	U78076	Mus musculus sepiapterin reductase gene, exons 1 and 2	1.8	2984225	(AE000766) enolase-phosphatase E-1 [Aquifex aeolicus]	0.095

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					COLLAGEN ALPHA 1(VIII)	
132	X52133	Paramecium 168G gene for 168G surface protein	1.8	115316	CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) >gi\|105686\|pir\|\|S15435 collagen alpha 1(VIII) chain precursor -	0.073
133	M77830	Human desmoplakin I mRNA, complete cds.	1.8	1397246	(U61944) coded for by C. elegans cDNA yk112f3.5; coded for by C. elegans cDNA cm21d2; coded for by C. elegans cDNA CEESR07F; coded for by C. elegans cDNA yk112f3.3; coded for by C. elegans cDNA CEESR29F [Caenorhabditis elegans]	1e-04
134	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.8	1353761	(U43192) myosin II heavy chain [Naegleria fowleri]	2e-05
135	AJ005518	Mus musculus somatostatin receptor 2 gene, exon1 and 5' flanking region	1.8	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nulcear division RFT1 protein (SP:P38206)	2e-08
136	AF002217	Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene, complete cds	1.8	3393018	(AL031174) hypothetical protein	2e-08
137	AF039035	Caenorhabditis elegans cosmid C53A3	1.8	3850109	(AL033388) 3-oxoacyl-[acyl-carrier-protein]-synthase	3e-11
138	M81769	S.domesticus immunoglobulin rearranged gamma chain mRNA, VJC region, complete cds.	1.8	3080527	(AL022600) putative mannose-1-phosphate gaunyl transferase [Schizosaccharomyces pombe]	3e-14
139	Y11106	P.pastoris PYC1 gene	1.8	1175412	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi\|984224 (Z54096) unknown	1e-15
140	U87803	Human putative Ca2+/calmodulin-dependent protein kinase kinase gene, 3' flanking region, partial sequence	1.8	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi\|2832633\|gnl\|PID\|e1249651 (AL021711) putative protein [Arabidopsis thaliana]	3e-17

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
141	AE001430	falciparum chromosome 2, section 67 of 73 of the complete sequence	1.8	1931647	(U95973) endomembrane protein EMP70 precusor isolog	2e-20
142	L19708	Rat N-methyl-D-aspartate receptor (NMDAR1) gene, first exon.	1.8	1731181	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi\|3874230\|gnl\|PID\|e1351618 protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans]	3e-21
143	Y10728	P.schwarzi mitochondrial cytb gene, partial	1.8	3878644	(Z81103) predicted using Genefinder; cDNA EST yk303g11.5 comes from this gene; cDNA EST yk303g11.3 comes from this gene [Caenorhabditis elegans]	1e-28
144	AB006631	Homo sapiens mRNA for KIAA0293 gene, partial cds	1.8	4176500	(AL031177) dJ889M15.3 (novel protein)	7e-45
145	AF106967	Mus musculus I3 protein mRNA, complete cds	1.7	<NONE>	<NONE>	<NONE>
146	AE001073	Archaeoglobus fulgidus section 34 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
147	U12977	Pseudomonas lemoignei poly(3-hydroxybutyrate) depolymerase A precursor (phaZ5) gene, complete cds, and glycerol-3-phosphate-dehydrogenase homolog, complete cds.	1.7	<NONE>	<NONE>	<NONE>
148	M27038	Mus musculus (SK/CamRk) germline IgK chain gene, J1-5 region.	1.7	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens HBF-1				
149	X74142	mRNA for transcription factor	1.7	<NONE>	<NONE>	<NONE>
150	U40830	Streptococcus thermophilus DeoD gene, partial cds and EpsA, EpsB, EpsC, EpsD, EpsE, EpsF, EpsG, EpsH, EpsI, EpsJ, EpsK, EpsL, EpsM, Orf14.9 protein genes, complete cds	1.7	<NONE>	<NONE>	<NONE>
151	L29172	Rabbit Ig germline gamma H-chain (allotype d12,e15) C-region gene, 3' end.	1.7	<NONE>	<NONE>	<NONE>
152	M19045	Human lysozyme mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
153	AE001159	Borrelia burgdorferi (section 45 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
154	L17027	Plasmid pFdA (from Fremyella diplosiphon) DNA sequence, including unidentified cds and stem loop.	1.7	<NONE>	<NONE>	<NONE>
155	U12232	Arabidopsis thaliana Columbia GTP binding protein beta subunit (AGB1) mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
156	D42056	Arabidopsis thaliana ATPK6 mRNA for ribosomal-protein S6 kinase homolog, complete cds	1.7	<NONE>	<NONE>	<NONE>
157	X98117	Rhizobium leguminosarum prsD, prsE, ORF3 genes	1.7	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
158	AF039084	Spinacia oleracea heat shock 70 protein protein, complete cds	1.7	<NONE>	<NONE>	<NONE>
159	Z12651	R.norvegicus gene for catechol methyltransferase	1.7	<NONE>	<NONE>	<NONE>
160	AF002968	Fringilla coelebs mitochondrial control region, partial sequence	1.7	<NONE>	<NONE>	<NONE>
161	AE001160	Borrelia burgdorferi (section 46 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
162	U67553	Methanococcus jannaschii section 95 of 150 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
163	M86247	S.ruminantium plasmid pS23 DNA.	1.7	<NONE>	<NONE>	<NONE>
164	S74436	oIL-8=interleukin-8 [sheep, spleen cells, mRNA, 1435 nt]	1.7	<NONE>	<NONE>	<NONE>
165	D12719	Candida maltosa ALK7 (CYP52A10) and ALK8 complete cds	1.7	<NONE>	<NONE>	<NONE>
166	U02625	Geotrichum candidum NRRL Y-553 lipase gene, partial cds.	1.7	321245	230k bullous pemphigoid antigen BPM1 - mouse	9.3
167	Z58881	H.sapiens CpG DNA, clone 114a4, reverse read cpg114a4.rt1a .	1.7	1854675	(U66298) bone morphogenetic protein-6 [Rattus norvegicus]	9.1
168	U43674	Agrobacterium tumefaciens conjugal transfer region 1 genes	1.7	1352066	LARGE PROLINE-RICH PROTEIN BAT2 MHC class III histocompatibility antigen HLA-B-associated transcript 2 - human >gi\|179339 (M33509) HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >gi\|179345 (M33518) HLA-B-associated transcript 2 (BAT2) [Homo sapiens]	9.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROTOPORPHYRINOGEN	
169	AL023827	Caenorhabditis elegans cosmid Y12A6A, complete sequence [Caenorhabditis elegans]	1.7	731440	OXIDASE (PPO) yeast (Saccharomyces cerevisiae) >gi\|603606 (U18778) Hem14p: protoporphyrinogen oxidase [Saccharomyces cerevisiae] >gi\|1403536\|gnl\|PID\|e249333 (Z71381) protoporphyrinogen oxidase [Saccharomyces cerevisiae]	8.9
170	X69662	X.laevis mRNA for glutathione synthetase, large subunit	1.7	4038057	(AC005897) hypothetical protein [Arabidopsis thaliana]	8.8
171	Z35824	S.cerevisiae chromosome II reading frame ORF YBL063w	1.7	3021450	(Y15515) prdl-a [Hydra vulgaris]	7.0
172	M65139	Cowpea chlorotic mottle virus (CCMV) 1a protein gene, complete cds.	1.7	2506307	COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR 1(XII) chain - chicken >gi\|222811\|gnl\|PID\|d1001160 gallus] >gi\|2326442\|gnl\|PID\|e39435 (X61024) collagen type XII alpha 1 chain [Gallus gallus]	7.0
173	X15065	Drosophila distal BX-C region (bithorax complex) pH189 5' region;	1.7	1723625	HYPOTHETICAL 10.0 KD PROTEIN IN ALPA-GABD INTERGENIC REGION (F87) >gi\|1033124 (U36840) ORF_f87 [Escherichia coli] >gi\|1788982 (AE000348) orf, hypothetical protein	6.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
174	Z46255	S.cerevisiae chromosome VI lambda clone.	1.7	3875228	(Z46792) similar to lethal(1) discs large-1 tumor suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB... >gi\|3879984\|gnl\|PID\|e1351767 suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB...	6.7
175	U01066	Human CD4 promoter, partial sequence.	1.7	125448	THYMIDINE KINASE saimiriine herpesvirus 1 (strain 11[Onc]) >gi\|60341	6.7
176	U34743	Phalaenopsis sp. 'hybrid SM9108' homeobox protein mRNA, complete cds	1.7	1022918	(U38184) ATPase subunit 6 [Trypanosoma cruzi]	6.7
177	U14662	Baboon herpesvirus HVP2 gB glycoprotein (UL27) gene, complete cds.	1.7	3218378	(AL023862) hypothetical protein SC3F9.07 [Streptomyces coelicolor]	6.7
178	AB017006	Homo sapiens PMS2L15 mRNA, partial cds	1.7	1465855	(U64859) glutamine-rich protein [Caenorhabditis elegans]	6.7
179	U92651	Brassica oleracea var. botrytis tonoplast intrinsic protein bobTIP26-1 mRNA, complete cds	1.7	3023675	DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein heavy chain [Schizosaccharomyces pombe]	6.6
180	AF000634	Lytechinus variegatus notch homolog mRNA, complete cds	1.7	148574	(M58520) endo-1,4-beta-glucanase [Fibrobacter succinogenes]	6.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
181	M92354	Arabidopsis thaliana anthranilate synthase alpha subunit gene, complete cds.	1.7	738308	blue light photoreceptor [Arabidopsis thaliana]	6.5
182	AJ234856	Hordeum vulgare genomic DNA fragment; clone MWG2234.rev	1.7	3142302	(AC002411) Strong similarity to myosin heavy chain gb\|Z34293 from A. thaliana. [Arabidopsis thaliana]	6.5
183	U76827	Stercorarius parasiticus bird J33 cytochrome b protein, partial cds	1.7	3413810	(Y17034) Bassoon [Mus musculus]	5.4
184	U05211	Saccharomyces cerevisiae Ttp1p (TTP1) gene, complete cds.	1.7	403173	(L24492) lipoprotein [Rhodococcus erythropolis]	4.9
185	AF076974	Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds	1.7	1170140	PUTATIVE ENDOGLUCANASE TYPE K PRECURSOR (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)	4.1
186	AE000753	Aquifex aeolicus section 85 of 109 of the complete genome	1.7	1169357	DNA ADENINE METHYLASE site-specific DNA-methyltransferase (adenine-specific) dam methylase gene product [Vibrio cholerae]	4.0
187	AF005638	Tupaia glis apolipoprotein AI prepropeptide mRNA, complete cds	1.7	3355682	(AL031124) putative secreted lyase	4.0
188	M23090	Human germline IgK chain gene V3-region, clone Humkv328h5	1.7	2257483	(AB004534) pi003 [Schizosaccharomyces pombe]	4.0
189	M24001	Mink enteritis virus antigenic type 2 capsid protein genes VP1 and VP2, complete cds.	1.7	2143504	myotonic dystrophy kinase - mouse (fragment) kinase, DM-kinase {C-terminal, alternatively spliced, clone delta II,III,IV,V} [mice, brain, Peptide Partial, 474 aa] [Mus sp.]	3.9
190	X59964	H.sapiens CST4 gene for Cystatin D	1.7	1766075	(U37273) winged helix protein CWH-2 [Gallus gallus]	3.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 11.7 KD	
191	X95276	P.falciparum complete gene map of plastid-like DNA (IR-B)	1.7	3219951	PROTEIN C6B12.13 IN CHROMOSOME I >gi\|2330843\|gnl\|PID\|e334047 pombe]	3.0
192	D84487	Rat PMSG-induced ovarian mRNA, 3'sequence, N10	1.7	173164	(J02719) valyl-tRNA synthetase [Saccharomyces cerevisiae]	2.3
193	L14851	Rattus norvegicus neurexin III-alpha gene, complete cds.	1.7	3323586	(AF060869) single-strand binding protein [Salmonella typhimurium]	2.3
194	M97002	Xenopus laevis/gilli hybrid pseudo-IgH chain gene, V region, clone LG7G342A.	1.7	2118407	MHC sex-limited protein - mouse (fragment) musculus]	2.3
195	L07025	Bacillus thuringiensis delta-endotoxin (CryA(a)) gene, 5' end. > :: gb\|I34520\|I34520 Sequence 1 from patent US 5596071 > :: gb\|I39790\|I39790 Sequence 1 from patent US 5616495 > :: gb\|AR008487\|AR008487 Sequence 1 from patent US 5753492	1.7	2496940	HYPOTHETICAL 53.4 KD PROTEIN D1054.13 IN CHROMOSOME V >gi\|3875316\|gnl\|PID\|e1344967	1.8
196	S73149	insulin-like growth factor II {intron 7} [human, Genomic, 1702 nt]	1.7	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	1.8
197	D86990	Human (lambda) DNA for immunoglobulin light chain	1.7	494367	Fv Fragment (Murine Se155-4) Complex With The Trisaccharide: Alpha-D-Galactose(1-2)[alpha-D-Abequose(1-3)]alpha- D-Mannose (P1-Ome) (Part Of The Cell-Surface Carbohydrate Of Pathogenic Salmonella)	1.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmid pFdA (from				
198	L17027	Fremyella diplosiphon) DNA sequence, including unidentified cds and stem loop.	1.7	1082702	poliovirus receptor-related protein - human	1.4
199	AL022273	Caenorhabditis elegans cosmid H22D14, complete sequence [Caenorhabditis elegans]	1.7	3924605	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]	1.4
200	U89926	Drosophila melanogaster cut gene, partial sequence	1.7	2245100	(Z97343) DNA-binding protein homolog	1.3
201	Z25749	H.sapiens gene for ribosomal protein S7	1.7	2493459	PROTEIN KINASE C SUBSTRATE, 60.1 KD PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN) >gi\|1215746	1.1
202	U59841	Fundulus heteroclitus lactate dehydrogenase B	1.7	3005587	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]	0.82
203	X55763	Rabbit mRNA for smooth muscle calcium channel blocker (CaCB) receptor	1.7	3883128	(AF082302) arabinogalactan-protein [Arabidopsis thaliana]	0.82
204	Z75528	Caenorhabditis elegans cosmid C18B12A, complete sequence [Caenorhabditis elegans]	1.7	940397	(D10123) core [Hepatitis C virus]	0.80
205	U50912	Human XIST gene, poly purine-pyrimidine repeat region	1.7	2338027	(AF005370) large tegument protein [Alcelaphine herpesvirus 1]	0.59
206	X12817	Ovis aries beta-lactoglobulin gene	1.7	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.45
207	AF004419	Homo sapiens troponin T (TNNT2) gene, exon 13	1.7	2996364	(AF053947) unknown [Yersinia pestis] >gi\|3883090	0.22
208	L43643	Gallus domesticus DNA microsatellite marker MCW119	1.7	464896	TRANSDUCIN-LIKE ENHANCER PROTEIN 1 enhancer-of-split homolog TLE-1 - human >gi\|307510	0.20

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
209	Z73278	S.cerevisiae chromosome XII reading frame ORF YLR106c	1.7	1351657	HYPOTHETICAL 123.9 KD PROTEIN C30D11.04C IN CHROMOSOME I >gi\|2130411\|pir\|\|S62562 hypothetical protein SPAC30D11.4c - fission yeast nuclear pore complex protein [Schizosaccharomyces pombe]	0.20
210	M22345	Mouse endogenous provirus gag, pol, and env region DNA.	1.7	2444455	(AF020765) hypothetical protein [Myxococcus xanthus]	0.12
211	AE000360	Escherichia coli K-12 MG1655 section 250 of 400 of the complete genome	1.7	2736361	(AF039038) No definition line found [Caenorhabditis elegans]	0.12
212	AB020692	Homo sapiens mRNA for KIAA0885 protein, complete cds	1.7	2605924	(AF029726) histidine kinase C [Dictyostelium discoideum]	0.094
213	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi\|1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.092
214	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi\|1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.088
215	U67205	Mus musculus ACF7 neural isoform 3 (mACF7) mRNA, partial cds	1.7	2047349	(AF000198) weak similarity to HSP90 [Caenorhabditis elegans]	0.052
216	X98188	Artificial DNA sequence for mammalian lambda-neo minichromosome, 1400 bp	1.7	2493779	PUTATIVE CUTICLE COLLAGEN C09G5.6 collagen; cDNA EST yk244c3.5 comes from this gene; cDNA EST yk244c3.3 comes from this gene [Caenorhabditis elegans]	0.042
217	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	1.7	2252630	(U95973) hypothetical protein [Arabidopsis thaliana]	0.041

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
218	L38808	Homo sapiens alpha-1 type V collagen (COL5A1) gene, 5' flank and exon 1.	1.7	2895760	(AF045246) universal minicircle sequence binding protein minicircle sequence binding protein [Crithidia fasciculata]	0.039
219	Z72151	B.napus mRNA for AMP-binding protein	1.7	190475	(K02576) salivary proline-rich protein 1 [Homo sapiens]	0.011
220	X94152	R.norvegicus mRNA for cysteine sulfinate decarboxylase	1.7	2136212	synapsin IIb - human >gi\|1594277 (U40215) synapsin IIb [Homo sapiens]	0.008
221	L20255	Mouse stathmin gene sequence.	1.7	2317934	(U97553) unknown [murine herpesvirus 68]	0.006
222	L13600	Rattus norvegicus glycine transporter mRNA, complete cds.	1.7	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	0.003
223	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.7	2072290	(U95094) XL-INCENP [Xenopus laevis]	0.001
224	S80642	butyrophilin [mice, lactating mammary gland, mRNA Partial, 3193 nt]	1.7	2695746	(AJ223010) Pmt2 [Schizosaccharomyces pombe]	9e-04
225	M22363	C.elegans unc-86 gene encoding two alternative proteins, complete cds.	1.7	2224683	(AB002369) KIAA0371 [Homo sapiens]	1e-04
226	X92123	M.musculus cgt gene exon 1	1.7	3874232	(Z49909) similar to Prokaryotic ribonuclease PH [Caenorhabditis elegans]	3e-05
227	AB016000	Ipomoea nil PKn2 (knotted-like gene) mRNA, complete cds	1.7	2183083	(AF000422) TTF-I interacting peptide 5 [Homo sapiens]	1e-05
228	D14133	Bovine mRNA for synaptocanalin I	1.7	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	2e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
229	L01991	Mus musculus TAFG-1-like neuronal glycoprotein (PCS) mRNA, complete cds.	1.7	3006139	(AL022299) hypothetical protein	4e-07
230	X63016	Tomato yellow leaf curl virus Thailand isolate complete genome (TYLCV-TH B-DNA)	1.7	3643608	(AC005395) hypothetical protein [Arabidopsis thaliana]	1e-07
231	Z22802	H.sapiens microsatellite repeat. > :: gb\|G34562\|G34562 human STS SHGC-51834	1.7	100210	extensin precursor (clone Tom L 4) - tomato esculentum]	4e-09
232	K02765	Human complement component C3 mRNA, alpha and beta subunits, complete cds.	1.7	2984320	(AE000773) acetoin utilization protein [Aquifex aeolicus]	1e-09
233	Z74818	S.cerevisiae chromosome XV reading frame ORF YOL076w	1.7	3873700	(Z73102) predicted using Genefinder; Similarity to Bacillus subtilis DNAJ protein gene; cDNA EST EMBL:C12520 comes from this gene; cDNA EST EMBL:D71409 comes from this ge...	7e-11
234	D21871	Pig mRNA for thimet oligopeptidase	1.7	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	8e-13
235	Y14344	Gallus gallus gene encoding neurofascin, exons 9,10,11 & 12	1.7	3876421	(Z81070) cDNA EST EMBL:C12730 comes from this gene; cDNA EST yk200b6.5 comes from this gene; cDNA EST yk349a12.5 comes from this gene [Caenorhabditis elegans]	3e-14
236	Z73608	S.cerevisiae chromosome XVI reading frame ORF YPL252c	1.7	1439663	(U64605) C05D9.6 gene product [Caenorhabditis elegans]	6e-18

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					OLIGOSACCHARYL	
237	AG000518	Homo sapiens genomic DNA, 21q region, clone: T171N23	1.7	1174468	TRANSFERASE STT3 SUBUNIT HOMOLOG >gi\|529357 (U13019) No definition line found [Caenorhabditis elegans]	6e-18
238	D17716	Human mRNA for N-acetylglucosaminyltransferase V, complete cds	1.7	961446	(D63877) KIAA0157 gene product is novel.	5e-19
239	AF102512	Cheilodactylus vittatus country USA: Midway Island cytochrome c oxidase subunit I gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.7	1572756	(U70848) C43G2.1 gene product [Caenorhabditis elegans]	5e-40
240	L30107	Rattus norvegicus liver-specific transporter gene, promoter region.	1.7	4176443	(AL022238) dJ1042K10.4 (novel protein)	3e-49
241	X91220	H.sapiens mRNA for Na-Cl electroneutral thiazide-sensitive cotransporter	1.7	3478637	(AC005546) R29425_1 [Homo sapiens]	6e-54
242	U97146	Rattus norvegicus calcium-independent phospholipase A2 mRNA, complete cds	1.6	<NONE>	<NONE>	<NONE>
243	Z48508	Pea seed-borne mosaic virus RNA for coat protein and polymerase (partial)	1.6	<NONE>	<NONE>	<NONE>
244	M18349	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5.	1.6	<NONE>	<NONE>	<NONE>
245	M13158	Yeast (S.pombe) cdc25+ gene (mitosis initiation), complete cds.	1.6	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mycoplasma				
246	U39712	genitalium section 34 of 51 of the complete genome	1.6	<NONE>	<NONE>	<NONE>
247	M17922	Mouse Murine urokinase-type plasminogen activator protein gene, complete cds.	1.6	3875750	(Z81499) predicted using Genefinder; cDNA EST yk410e3.3 comes from this gene; cDNA EST yk410e3.5 comes from this gene [Caenorhabditis elegans]	8.0
248	M89986	Human polymorphic loci in Xq28.	1.6	3261710	(Z84724) psd [Mycobacterium tuberculosis]	6.4
249	M89986	Human polymorphic loci in Xq28.	1.6	2143805	inositol-polyphosphate 4-phosphatase - rat	6.2
250	U68725	Rattus norvegicus Deleted in colorectal Cancer	1.6	1256804	(U51449) RING3 protein [Xenopus laevis]	5.8
251	X95199	P.platessa GSTA, GSTA1, GSTA2, and PPTN genes	1.6	3915113	MALEYLACETATE REDUCTASE Pseudomonas cepacia >gi\|643636 (U19883) maleylacetate reductase [Burkholderia cepacia]	4.9
252	Y09103	D.melanogaster RPA1 gene	1.6	3916021	HYPOTHETICAL 91 KD PROTEIN IN COB INTRON >gi\|2654230\|gnl\|PID\|e1192341 (X02819) unidentified reading frame [Schizosaccharomyces pombe]	4.8
253	Z14078	T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA	1.6	2501668	DYSTROPHIN-RELATED PROTEIN 2 sapiens]	3.6
254	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.6	130997	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 1 PRECURSOR >gi\|81809\|pir\|\|A29324 proline-rich protein precursor - soybean >gi\|170049 (J02746) proline-rich protein [Glycine max]	2.8
255	M21488	Human muscle creatine kinase gene (CKMM), exon 2.	1.6	119399	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP40]	2.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
256	AE001164	Borrelia burgdorferi (section 50 of 70) of the complete genome	1.6	4050089	(AF109907) hypothetical protein [Homo sapiens]	1.5
257	X61757	M.musculus rearranged T-cell receptor beta variable region (Vb17a)	1.6	3377766	(AF080090) semaphorin IV isoform b [Mus musculus]	1.2
258	M15346	T.cruzi tandemly repeated gene encoding an 85 kDa antigen with homology to heat shock proteins.	1.6	2804437	(AF043695) similar to zinc metalloprotease family of peptidases [Caenorhabditis elegans]	0.41
259	L39018	Rattus norvegicus sodium channel protein 6 (SCP6) mRNA, complete cds	1.6	2920535	(AF018081) type XVIII collagen [Homo sapiens]	0.037
260	M29483	Human leukocyte adhesion protein p150,95 alpha subunit gene, exons 7 - 15.	1.6	1840045	(U49082) transporter protein [Homo sapiens]	2e-09
261	L06844	Aspergillus niger beta-D-fructofuranosidase (suc1) gene, one exon.	1.6	4206210	(AF071527) putative calcium channel [Arabidopsis thaliana]	9e-10
262	M10946	Chicken aldolase B gene, complete cds, clones lambda-C(11.1,4).	1.6	2746775	(AF040640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]	1e-31
263	X07881	Human gene PRB3L for proline-rich protein G1	1.5	<NONE>	<NONE>	<NONE>
264	U22260	Nicotiana tabacum UMP synthase (pyr5-6) mRNA, partial cds	1.5	3880923	(Z99271) similar to Reverse transcriptase comes from this gene [Caenorhabditis elegans]	0.50
265	U76759	Mus musculus nuclear protein NIP45 mRNA, complete cds	1.4	1330394	(U58761) C01F1.6 gene product [Caenorhabditis elegans]	8.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					POTASSIUM-TRANSPORTING ATPASE BETA CHAIN (PROTON PUMP) (GASTRIC H+/K+ ATPASE BETA SUBUNIT) 3.6.1.36) beta chain - human >gi\|184105 (M75110) H,K-ATPase beta subunit [Homo sapiens]	
266	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	1.4	1703461		8.9
267	X64659	C.jacchus interferon gene for interferon gamma	1.4	1486485	(U28832) US10 [Gallid herpesvirus 1] >gi\|1486497	6.8
268	U11825	Schistosoma japonicum structural muscle protein paramyosin mRNA, complete cds.	0.88	<NONE>	<NONE>	<NONE>
269	D84278	Human DNA for CD38, exon 1	0.68	3766363	(AL031907) hypothetical serine rich protein [Schizosaccharomyces pombe]	3.0
270	M59755	Bovine lens aldose reductase pseudogene, 3' end.	0.67	<NONE>	<NONE>	<NONE>
271	M81758	Homo sapiens skeletal muscle voltage-dependent sodium channel alpha subunit (SkM1) mRNA, complete cds.	0.65	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.6
272	L01965	Human type IV sodium channel alpha polypeptide	0.64	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.5
273	U90122	Danio rerio bone morphogenetic protein-4 (bmp4) mRNA, partial cds	0.63	2983532	(AE000720) formate dehydrogenase alpha subunit [Aquifex aeolicus]	7.9
274	L41624	Hylobates lar mucin (MUC1) gene, exons 1-6.	0.63	1517808	(D79215) FGF-10 [Rattus norvegicus]	0.91

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U67956) coded for by C.	
275	AF030881	Fugu rubripes sushi retrotransposon gag polyprotein (gag) and pol polyprotein (pol) genes, complete cds	0.63	1519696	elegans cDNA yk126f9.5; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5 [Caenorhabditis elegans]	0.38
276	U52909	Arabidopsis thaliana U1 snRNP 70K protein gene, complete cds	0.62	<NONE>	<NONE>	<NONE>
277	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA, complete cds	0.62	3800934	(AF100655) contains similarity to ser/thr protein kinases [Caenorhabditis elegans]	9.7
278	U17081	Human fatty acid binding protein (FABP3) gene, complete cds	0.62	3617848	(AF049709) tyrosylprotein sulfotransferase-A; TPST-A	7.7
279	AB018340	Homo sapiens mRNA for KIAA0797 protein, partial cds	0.62	424044	VP5 protein - porcine rotavirus >gi\|61355	7.7
280	Y00093	H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.62	1054945	(U38621) polyprotein [Tobacco vein mottling virus]	4.5
281	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	0.62	136810	GLYCOPROTEIN M >gi\|73791\|pir\|\|WMBE51 UL10 protein - human herpesvirus 1 1-473) [Human herpesvirus 1] >gi\|221732\|gnl\|PID\|d1002131	3.5
282	X76056	N. sylvestris DNA for spacer region between 25S and 18S ribosomal RNA genes	0.62	2661176	(U76671) putative cds [Rhodobacter sphaeroides]	2.0
283	X74501	B.taurus mRNA for ACTH receptor	0.62	4249552	(AB001075) galectin-2 related protein	2.0
284	M57634	Rat F1-ATPase beta subunit mRNA, 3' end.	0.62	2119692	transforming growth factor-beta type III receptor - chicken >gi\|511843 (L01121) transforming growth factor-beta type III receptor [Gallus gallus]	1.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ASPARTYL/ASPARAGINYL	
285	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	0.62	2498164	BETA-HYDROXYLASE (ASPARTATE BETA-HYDROXYLASE) (ASP BETA-HYDROXYLASE) (PEPTIDE-ASPARTATE BETA-DIOXYGENASE) beta-dioxygenase (EC 1.14.11.16) - bovine >gi\|162694 taurus]	0.52
286	AL010142	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence	0.62	3183206	HYPOTHETICAL PROTEIN KIAA0009 sapiens]	4e-07
287	AB008160	Mus musculus Stat3 gene, 5'-flanking region and exon 1 partial sequence	0.62	466097	HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III >gi\|1078903\|pir\|\|S44654 ZK353.1 protein - Caenorhabditis elegans >gi\|289757 (L15313) putative [Caenorhabditis elegans]	1e-35
288	AB018795	Halomonas marina gene for alginate lyase, complete cds	0.62	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4...	3e-46
289	Z69906	Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.61	<NONE>	<NONE>	<NONE>
290	U18259	Human clone CIITA-8 MHC class II transactivator CIITA mRNA, complete cds.	0.61	1483567	(X79983) viral proteinase [Pseudorabies virus]	9.8
291	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.61	475724	(U08884) protein VIII precursor [Bovine adenovirus type 3]	7.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
292	U70825	Rattus norvegicus 5-oxo-L-prolinase mRNA, complete cds	0.61	733543	(U23448) similar to genome polyprotein (SP:POLG_BVDVN, P19711); alternative splicing to C04A2.7a	4.4
293	L81667	Homo sapiens (subclone 2_a9 from P1 H49) DNA sequence	0.61	2565087	(U80759) CAGH4 alternate open reading frame [Homo sapiens]	3.3
294	AE000760	Aquifex aeolicus section 92 of 109 of the complete genome	0.61	2811092	HOMEOBOX PROTEIN HOX-A3 (HOX-1.5) homeobox-containing transcription factor [Mus musculus]	2.6
295	U58512	Mus musculus Rho-associated, coiled-coil forming protein kinase p160 ROCK-1 mRNA, complete cds	0.61	295671	(L11275) selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III	1.5
296	U27459	Human origin recognition complex protein 2 homolog hORC2L mRNA, complete cds	0.61	200285	(M97900) putative open reading frame [Mus musculus]	0.66
297	L36680	Pisum sativum S-adenosylmethionine synthase mRNA, 3' end.	0.61	2285790	(AB002086) p47 [Rattus norvegicus]	4e-12
298	AE000673	Aquifex aeolicus section 5 of 109 of the complete genome	0.61	3395782	(AF058446) histone macroH2A1.2 [Gallus gallus]	6e-27
299	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	0.61	3646450	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]	8e-29
300	AJ009675	Agrotis ipsilon mRNA for 3-hydroxy-3-methylglutaryl coenzyme A reductase	0.61	4176370	(AC005058) similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	2e-73
301	AC005577	Homo sapiens chromosome 19, cosmid F18382B, centromeric end, complete sequence [Homo sapiens]	0.60	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Candida albicans				
302	U40454	topoisomerase type I (CATOP1) gene, complete cds	0.60	<NONE>	<NONE>	<NONE>
303	J01390	Emericella nidulans mtDNA between h2/h5 and bh2/b2 junctions. genes for ATPase subunit 6, cytochrome oxidase subunit 3, seven. unidentified proteins, twentyfour tRNA's and L-rRNA.	0.60	<NONE>	<NONE>	<NONE>
304	L11172	Plasmodium falciparum RNA polymerase I gene, complete cds.	0.60	<NONE>	<NONE>	<NONE>
305	Z81079	Caenorhabditis elegans cosmid F39H11, complete sequence [Caenorhabditis elegans]	0.60	<NONE>	<NONE>	<NONE>
306	Z49627	S.cerevisiae chromosome X reading frame ORF YJR127c	0.60	118751	MAJOR DNA-BINDING PROTEIN herpesvirus 1 (strain 11) >gi\|60327 (X64346) major ssDNA-binding protein [Saimiriine herpesvirus 2]	9.6
307	U94911	Rattus norvegicus H-K-ATPase alpha 2 gene, alternatively spliced products and partial cds	0.60	2213862	(AF003086) PfSNF2L [Plasmodium falciparum]	7.4
308	U67476	Methanococcus jannaschii section 18 of 150 of the complete genome	0.60	1749688	(D89240) unnamed protein product	5.7
309	U67513	Methanococcus jannaschii section 55 of 150 of the complete genome	0.60	3327421	(U97068) zonadhesin [Mus musculus]	4.3
310	U57817	Haemophilus ducreyi lipoprotein gene, complete cds	0.60	4008577	(AL034491) conserved hypothetical protein [Schizosaccharomyces pombe]	2.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					probable protein-tyrosine kinase	
311	X80700	H.sapiens G17 gene	0.60	422541	(EC 2.7.1.112) RTK - Pacific electric ray >gi\|290858	1.5
312	L42167	Mus musculus (clone R24) rds gene, partial cds	0.60	4220848	(AF033823) moira [Drosophila melanogaster]	0.51
313	U54777	Human hMSH6 mRNA, complete cds	0.60	2665637	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07
314	D86985	Human mRNA for KIAA0232 gene, complete cds	0.60	1938462	(U97006) No definition line found [Caenorhabditis elegans]	2e-07
315	D43964	Rat liver mRNA for Kan-1, complete cds	0.60	1280135	(U55376) coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	5e-15
316	U49058	Rattus norvegicus CTD-binding SR-like protein rA4 mRNA, partial cds	0.60	2145091	(U37500) RNA polymerase II largest subunit [Mus musculus]	1e-19
317	X84388	U.ruddi mitochondrial 12S ribosomal RNA	0.60	3874247	(Z70205) predicted using Genefinder	2e-37
318	AF125447	Caenorhabditis elegans cosmid Y14H12B	0.59	<NONE>	<NONE>	<NONE>
319	U20189	Hyoscyamus muticus clone cVS2 vetispiradiene synthase mRNA, partial cds.	0.59	<NONE>	<NONE>	<NONE>
320	M63962	Human gastric H,K-ATPase catalytic subunit gene, complete cds.	0.59	<NONE>	<NONE>	<NONE>
321	AJ132366	Helicobacter pylori (strain P1) comB and pmi/algA (partial) genes, and partial ORF1 and ORF2	0.59	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
322	U17289	transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.59	2459419	(AC002332) hypothetical protein [Arabidopsis thaliana]	9.4
323	Z71466	S.cerevisiae chromosome XIV reading frame ORF YNL190w	0.59	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	7.3
324	Z66493	Beet soil-borne virus genes for 13K, 22K and 48K proteins	0.59	2119867	cryV465 protein - Bacillus thuringiensis thuringiensis]	7.2
325	L41351	Homo sapiens prostasin mRNA, complete cds	0.59	729212	CRYSTALLIN J1C crystallin [Tripedalia cystophora]	4.2
326	X79854	S.lincolnensis gene for 16S ribosomal RNA	0.59	3702828	(AF056577) high mobility group protein 1.2	3.2
327	AJ223356	Strongylocentrotus purpuratus mRNA for SuDp98 protein	0.59	2495704	HYPOTHETICAL PROTEIN KIAA0129 product is novel. [Homo sapiens]	2.5
328	X86019	H.sapiens mRNA for PRPL-2 protein	0.59	1743341	(Y10027) transcription factor TEF-1 [Mus musculus]	2.5
329	U75528	Xiphias gladius creatine kinase gene, partial cds	0.59	1845995	(U69477) envelope glycoprotein [Human immunodeficiency virus type 1]	2.4
330	AC005573	Homo sapiens chromosome 5, PAC clone 202e13	0.59	2506366	DNA POLYMERASE EPSILON SUBUNIT B DNA-directed DNA polymerase (EC 2.7.7.7) II chain B - yeast (Saccharomyces cerevisiae) >gi\|786319 (U25842) DNA Polymerase epsilon, subunit B (Swiss Prot. accession number P24482) [Saccharomyces cerevisiae]	1.4
331	L19180	Rat receptor-linked protein tyrosine phosphatase	0.59	1235974	(X96713) collagen [Globodera pallida]	1.1
332	L32090	Listeria monocytogenes secA gene, complete cds.	0.59	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.83

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis			(AL031124) hypothetical	
333	U24433	syndecan-2 mRNA, complete cds.	0.59	3355692	protein SC1C2.25c [Streptomyces coelicolor]	0.64
334	M23412	Drosophila muscarinic acetylcholine receptor mRNA, complete cds.	0.59	168237	(M76546) hydroxyproline-rich protein [Helianthus annuus]	0.22
335	AF060729	Synaphea media chloroplast atpB-rbcL intergenic spacer region, partial sequence	0.59	731596	HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION >gi\|626567\|pir\|\|S46825 hypothetical protein YHL010c - yeast (Saccharomyces cerevisiae) >gi\|2289881 (U11582) No definition line found [Saccharomyces cerevisiae]	0.16
336	AF029734	Xanthobacter autotrophicus transcriptional activator AldR (aldR) gene, partial cds; and NAD-dependent chloroacetaldehyde dehydrogenase (aldB) gene, complete cds	0.59	2498801	PERIAXIN >gi\|2143901\|pir\|\|I58157 periaxin - rat >gi\|505297 (Z29649) periaxin [Rattus norvegicus]	0.13
337	X95307	C.reinhardtii LI818r-1 gene	0.59	1723781	HYPOTHETICAL 34.3 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION >gi\|2131717\|pir\|\|S64612 hypothetical protein YGR277c - yeast (Saccharomyces cerevisiae) >gi\|1323505\|gnl\|PID\|e243248 (Z73062) ORF YGR277c [Saccharomyces cerevisiae]	1e-04
338	M24572	Dictyostelium discoideum tRNA-Glu-GAA gene, clone yGluGAA8.	0.59	1176186	HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION >gi\|606121 coli]	3e-06
339	U73733	Human hMSH6 gene, exon 2	0.59	2665637	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Escherichia coli				
340	D90747	genomic DNA. (25.2 - 25.6 min)	0.59	134286	DOLICHOL KINASE	6e-08
341	J05211	Human desmoplakin mRNA, 3' end.	0.59	246796	major centromere protein, CENP-B [human, Peptide, 594 aa]	4e-08
342	L24441	Loligo pealii kinesin light chain mRNA, complete cds.	0.59	547800	KINESIN LIGHT CHAIN (KLC) sea urchin (Strongylocentrotus purpuratus) >gi\|161530	5e-14
343	M25140	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4.	0.58	<NONE>	<NONE>	<NONE>
344	L81932	Homo sapiens (subclone 9_h2 from P1 H21) DNA sequence	0.58	<NONE>	<NONE>	<NONE>
345	AF087966	Homo sapiens full length insert cDNA clone YU51G04	0.58	<NONE>	<NONE>	<NONE>
346	Z78574	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10G11	0.58	<NONE>	<NONE>	<NONE>
347	AF068061	Blattella germanica allatostatin neuropeptide precursor, gene, complete cds	0.58	<NONE>	<NONE>	<NONE>
348	AF015592	Homo sapiens Cdc7 (CDC7) mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
349	AF028006	Methanosarcina barkeri atp operon: ATP synthase beta subunit (atpD), ATP synthase epsilon subunit (atpC), ATP synthase gene 1 (atpI), ATP synthase a subunit subunit (...	0.58	3184291	(AC004136) putative DNA polymerase III gamma subunit	9.4
350	AB017032	Mus musculus gene for pancreatic trypsin, complete cds	0.58	3170561	(AF056704) synapsin IIIa [Rattus norvegicus]	9.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Dictyostelium				
351	AF081585	discoideum developmental protein DG1110 (DG1110) gene, partial cds	0.58	105417	basic proline-rich peptide IB-8a - human	9.2
352	AF086322	Homo sapiens full length insert cDNA clone ZD53E01	0.58	93026	hypothetical protein - African swine fever virus (strain Malawi Lil-20/1) >gi\|450758 (X71982) myeloid differentiation antigen homologue [African swine fever virus] >gi\|903686 (M95672) unknown protein	7.1
353	AF088025	Homo sapiens full length insert cDNA clone ZC19C04	0.58	2384644	(U92805) thrombospondin-3 [Xenopus laevis]	7.0
354	AB002339	Human mRNA for KIAA0341 gene, partial cds	0.58	2135587	M130 antigen (cytosolic variant 2) - human	5.4
355	U67548	Methanococcus jannaschii section 90 of 150 of the complete genome	0.58	2911094	(AL021957) hypothetical protein Rv2174	4.2
356	L07868	Homo sapiens receptor tyrosine kinase (ERBB4) gene, complete cds.	0.58	461922	PYRUVATE DECARBOXYLASE (8-10 NM CYTOPLASMIC FILAMENT-ASSOCIATED PROTEIN) (P59NC) 4.1.1.1) - Neurospora crassa >gi\|293948 (L09125) pyruvate decarboxylase [Neurospora crassa] >gi\|1655909	4.2
357	X03897	Bacillus subtilis sigma 43 operon with P23-dnaE-rpoD genes (dnaE for DNA primase, rpoD for RNA polymerase)	0.58	1323704	(U55387) similar to C. elegans F38E1.9 gene product encoded by GenBank Accession Number U41996 [Cricetulus griseus]	4.1
358	D76419	Desulfovibrio vulgaris rbo gene for desulfoferrodoxin and rub gene for rubredoxin, complete cds	0.58	3420047	(AC004680) putative protein kinase [Arabidopsis thaliana]	2.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA sequence from cosmid B20F6 on chromosome 22, complete sequence [Homo sapiens]	0.58	2145455	(Y07866) catalase-peroxidase	2.4
359	Z82174					
360	M33642	F.solani STI35 protein gene, complete cds.	0.58	2896706	(AL021897) hypothetical protein Rv1069c	2.4
361	U64873	Mus musculus transforming growth factor alpha (TGF alpha) gene, partial cds	0.58	3874437	(Z81038) predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene [Caenorhabditis elegans]	1.8
362	AB002132	Macrophthalmus banzai mitochondrial DNA for 12S and 16S rRNA, partial and complete sequence	0.58	2960022	(AJ224676) rho type GEF [Drosophila melanogaster]	1.8
363	AF070070	Caenorhabditis elegans MutS homolog (msh-5) mRNA, partial cds	0.58	4098205	(U75869) Omp22 [Helicobacter pylori]	1.8
364	AF045240	Staphylococcus epidermidis plasmid pIP1629 mobilization protein (mobC1), (orf69-1), (mobA1),	0.58	4218117	(AL035353) protein (fragment)	0.62
365	X61637	H.sapiens Wilms tumor gene 1, exons 8 and 9	0.58	2331059	(U88211) unknown [Gallus gallus]	0.62
366	AF039312	Moraxella catarrhalis strain 4223 transferrin binding protein A (tbpA) and transferrin binding protein B (tbpB) genes, complete cds; and unknown gene	0.58	120155	FIBER PROTEIN >gi\|74229\|pir\|\|ERADFM fiber protein - mouse adenovirus 1 >gi\|209758 (M30594) fiber protein [Mastadenovirus mus1]	0.27
367	D87463	Human mRNA for KIAA0273 gene, complete cds	0.58	3861477	(U94177) androgen receptor [Pan troglodytes]	0.12
368	U40342	Mus musculus ninein mRNA, complete cds.	0.58	4115936	(AF118223) No definition line found [Arabidopsis thaliana]	0.004

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
369	S57235	CD68=110kda transmembrane glycoprotein [human, promonocyte cell line U937, mRNA, 1722 nt]	0.58	2072501	(U96113) WWP1 [Homo sapiens]	1e-04
370	U39391	Mus musculus serotonin1A receptor mRNA, complete cds.	0.58	1469876	(D63481) The KIAA0147 gene product is related to adenylyl cyclase. [Homo sapiens]	1e-07
371	D00056	Monkey B-lymphotropic papovavirus genes for VP-1, 2, 3 and large T antigen, complete and partial cds, strain LPV-76 > :: gb\|M14494\|PPMVP1 M Monkey B-lymphotropic papovavirus mutant (LPV-76) PstI B fragment encoding VP1, VP2, VP3 and T-antigen.	0.58	2462069	(AJ001774) vanadium chloroperoxidase	1e-08
372	M77182	Amsacta entomopoxvirus spheroidin gene, complete cds, and four vaccinia related orfs. > :: gb\|I16670\|I16670 Sequence 1 from patent US 5476781	0.58	1730722	HYPOTHETICAL 43.8 KD PROTEIN IN NCE3-HHT2 INTERGENIC REGION >gi\|2131871\|pir\|\|S62957 hypothetical protein YNL035c - yeast (Saccharomyces cerevisiae) >gi\|1301880\|gnl\|PID\|e239670 (Z71311) ORF YNL035c [Saccharomyces cerevisiae]	8e-14
373	S72579	igloo-S=growth-associated protein GAP-43 homolog	0.58	2689720	(AF037168) DnaJ homologue [Arabidopsis thaliana]	7e-14
374	AF018165	Tetraodon fluviatilis amyloid precursor protein mRNA, complete cds	0.58	3219938	HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I >gi\|2058378\|gnl\|PID\|e314002 pombe]	5e-22

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
375	U81803	Filobasidiella neoformans translation elongation factor EF1-alpha (CnTEF1) mRNA, complete cds	0.57	<NONE>	<NONE>	<NONE>
376	U09781	Candida albicans ATCC 18804, CBS 562 peptide transporter gene, complete cds.	0.57	<NONE>	<NONE>	<NONE>
377	AC002143	Homo sapiens (subclone 4_b10 from BAC H102) DNA sequence	0.57	<NONE>	<NONE>	<NONE>
378	U23442	Tetrahymena thermophila RR internal deletion sequence.	0.57	<NONE>	<NONE>	<NONE>
379	U17289	Mus musculus transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.57	<NONE>	<NONE>	<NONE>
380	X70844	Buzura suppressaria nuclear polyhedrosis virus gene for polyhedrin protein	0.57	<NONE>	<NONE>	<NONE>
381	AJ012159	Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene	0.57	<NONE>	<NONE>	<NONE>
382	X76571	H.sapiens simple DNA sequence region clone wg1a8.	0.57	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
383	AF034434	Vibrio cholerae pathogenicity island, putative transposase, aldehyde dehydrogenase (aldA), toxR-activated gene A protein (tagA), putative inner membrane protein, and putative zinc metalloprotease genes, complete cds; and...	0.57	<NONE>	<NONE>	<NONE>
384	AB017031	Mus musculus gene for TESP4, complete cds	0.57	<NONE>	<NONE>	<NONE>
385	X89788	S.hispidus mitochondrial DNA for SSU ribosomal RNA gene	0.57	<NONE>	<NONE>	<NONE>
386	L16921	Rat progesteron receptor gene, 5' untranslated region.	0.57	3323116	(AE001251) femA protein, putative [Treponema pallidum]	8.9
387	AF027292	Homo sapiens interferon regulatory factor 6	0.57	259790	(S48157) DNA polymerase-primase 180 kda subunit [Drosophila melanogaster, Peptide, 1490 aa]	6.7
388	AJ012581	Cicer arietinum mRNA for cytochrome P450	0.57	2131498	hypothetical protein YDR446w - yeast CAI: 0.11 [Saccharomyces cerevisiae]	5.3
389	L15363	Human transfer RNA-Met (TRMEP1) pseudogene, complete gene	0.57	3228680	(AF070935) GABA receptor subunit [Musca domestica]	5.2
390	AE000525	Helicobacter pylori 26695 section 3 of 134 of the complete genome	0.57	1938478	(U97008) weak similarity to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	4.0
391	AF020189	Amblyomma americanum ecdysteroid receptor (AamEcR) mRNA, 3'UTR, region 1	0.57	2072224	(U94875) p40 [Borna disease virus]	4.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human UbA52 gene				
392	X56997	coding for ubiquitin-52 amino acid fusion protein	0.57	2960113	(AL022121) hypothetical protein Rv3689	4.0
393	AL010260	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-81, complete sequence	0.57	117233	CYTOCHROME P450 2C14 (CYPIIC14) phenobarbital-inducible, hepatic - rabbit P-450 [Oryctolagus cuniculus] >gi\|358265\|prf\|\|1306317A cytochrome P450 [Oryctolagus cuniculus]	3.9
394	M99581	Xenopus laevis gamma-crystallin (gcry3) gene, complete cds.	0.57	141647	GASTRULA ZINC FINGER PROTEIN XLCGF44.2 >gi\|85736\|pir\|\|S06571 finger protein (clone XlcGF44-2) - African clawed frog (fragment)	3.0
395	M38384	Drosophila melanogaster seven in absentia mRNA, complete cds.	0.57	1707127	(U80454) T16A1.1 [Caenorhabditis elegans]	3.0
396	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.57	1173433	IRON(III)-TRANSPORT SYSTEM PERMEASE PROTEIN SFUB >gi\|152861 (M33815) protein (sufB)	2.3
397	X12600	Klebsiella pneumoniae nifX, nifU, nifS, nifV and nifW genes	0.57	2909562	(AL021925) hypothetical protein Rv2256c	1.4
398	AB014526	Homo sapiens mRNA for KIAA0626 protein, complete cds	0.57	482390	insect-stage-specific protein - Trypanosoma cruzi >gi\|162099 (M65021) insect stage-specific antigen	0.61
399	AF063587	Rhodococcus fascians strain NRRL-B-15096 hypothetical protein gene, complete cds	0.57	4104321	(AF034582) vesicle associated protein [Rattus norvegicus]	0.46
400	L11117	Guinea pig estrone sulfotransferase gene.	0.57	82584	alpha/beta-gliadin precursor (clone A212) - wheat	0.35

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
401	V00829	Mouse complete gene for a mouse kallikrein gene. Genes are mGK-1 (complete gene) and mGK-2 of hormones, e.g., grow... > :: gb\|J00390\|MUSKAL 07 Mouse pseudo-kallikrein 2, exons 4 and 5, and kallikrein 1 gene, complete cds.	0.57	2500916	NUCLEAR HORMONE RECEPTOR NOR-2 receptor [Rattus norvegicus] >gi\|1583604\|prf\|\|2121281A NOR-2 protein [Rattus norvegicus]	0.20
402	X53092	Chicken mRNA for beta-2 subunit of neuronal nicotinic acetylcholine receptor	0.57	1072256	(U40953) similar to matrin F/G (SP:Q00910) containing C4-type zinc-fingers [Caenorhabditis elegans]	0.031
403	L07939	Ovis ovis granulocyte colony stimulating factor	0.57	3874345	(Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes f...	3e-07
404	U18061	Colletotrichum gloeosporioides CAP20 (cap20) gene, complete cds.	0.57	2914695	(AC003974) putative ubiquitin specific protease	9e-08
405	Z73955	L.japonicus mRNA for small GTP-binding protein, RAB11G	0.57	112894	TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) >gi\|107549\|pir\|\|A35797 probable DNA-binding protein A20 - human >gi\|177866 (M59465) A20	7e-08

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
406	X04335	Petunia grp-1 gene for glycine-rich protein	0.57	3876901	(Z77660) Similarity to Human enoyl-CoA hydratase (SW:ECHM_HUMAN); cDNA EST EMBL:T00611 comes from this gene; cDNA EST yk203d10.3 comes from this gene; cDNA EST yk203d10.5 comes from this gene; cDNA EST yk457h5.3 comes from t...	1e-27
407	U40718	Rattus norvegicus S-adenosylmethionine decarboxylase (AMDP2) pseudogene	0.56	<NONE>	<NONE>	<NONE>
408	M60318	S.cerevisiae SSD1 protein gene, complete cds. > :: gb\|AR013983\|AR013983 Sequence 8 from patent US 5773245	0.56	<NONE>	<NONE>	<NONE>
409	X60057	Nicotiana tabacum blp4 mRNA for luminal binding protein (BiP)	0.56	<NONE>	<NONE>	<NONE>
410	AF085930	Homo sapiens full length insert cDNA clone YR55A09	0.56	<NONE>	<NONE>	<NONE>
411	AL010189	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-102, complete sequence	0.56	<NONE>	<NONE>	<NONE>
412	X05402	Murine G-CSF gene for granulocyte colony stimulating factor precursor	0.56	<NONE>	<NONE>	<NONE>
413	U92280	Rattus norvegicus regulator of G-protein signalling 12 (RGS12) mRNA, complete cds	0.56	<NONE>	<NONE>	<NONE>
414	U85660	Human papillomavirus strain RTRX7 complete genome	0.56	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
415	X57626	M. javanica mitochondrion ATPase 6, and putative tRNA-f-Met and tRNA-His genes	0.56	<NONE>	<NONE>	<NONE>
416	AB003363	Sus scrofa S100C gene, complete cds	0.56	<NONE>	<NONE>	<NONE>
417	L42291	Danio rerio DANA element, intron 4.	0.56	2650002	(AE001062) conserved hypothetical protein [Archaeoglobus fulgidus]	8.7
418	AF031826	Mus musculus leukocystatin gene, complete cds	0.56	462493	L-LACTATE DEHYDROGENASE (IMMUNOGENIC PROTEIN P36) >gi\|479296\|pir\|\|S33362 L-lactate dehydrogenase (EC 1.1.1.27) - Mycoplasma hyopneumoniae	6.7
419	U17068	Pennisetum glaucum Ac-like element, AcL2.	0.56	399449	ESCARGOT/SNAIL PROTEIN HOMOLOG	6.7
420	Z48042	H.sapiens mRNA encoding GPI-anchored protein p137	0.56	141232	HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D) >gi\|76316\|pir\|\|QQSA7C hypothetical protein E-74	6.7
421	AF027657	Choristoneura fumiferana entomopoxvirus nucleotide triphosphate phosphohydrolase I (NPHI) gene, complete cds	0.56	464999	PUTATIVE ACETYLCHOLINE REGULATOR UNC-18 >gi\|480359\|pir\|\|S36747 acetylcholine regulator unc-18 - Caenorhabditis elegans >gi\|247392\|bbs\|100294 putative acetylcholine regulator unc-18	5.1
422	AB011540	Homo sapiens mRNA for MEGF7, partial cds	0.56	1718033	URACIL-DNA GLYCOSYLASE (UDG) herpesvirus 2 >gi\|695219 (U20824) uracil DNA glycosylase	5.1
423	X59941	X.maculatus NGF gene for nerve growth factor	0.56	1169081	COMMON PLANT REGULATORY FACTOR CPRF-1 >gi\|515621 (X58575) light-inducible protein CPRF-1 [Petroselinum crispum] >gi\|1498301 (U46217) CPRF1	3.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
424	M72711	Rat transcriptional repressor of myelin-specific genes (SCIP) mRNA, complete cds.	0.56	501027	(U01849) ORF2 [Trypanosoma brucei]	2.3
425	AL023850	Caenorhabditis elegans cosmid Y67D11A, complete sequence [Caenorhabditis elegans]	0.56	266771	CHORISMATE MUTASE (CM) / PREPHENATE DEHYDRATASE (PDT) (P-PROTEIN) >gi\|281791\|pir\|\|S26053 chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51) - Erwinia herbicola >gi\|43344	2.3
426	U47862	Schistosoma mansoni gynecophoral canal protein mRNA, complete cds	0.56	2147138	ATP synthase chain 6 - Platymonas subcordiformis mitochondrion >gi\|633582 (Z47797) ATP synthase subunit 6 [Platymonas subcordiformis]	2.3
427	V00574	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons.	0.56	1518672	(U60289) receptor protein tyrosine phosphatase psi [Homo sapiens]	1.7
428	Z71502	X.laevis H1(0)-1 gene	0.56	1651674	(D90899) ferrichrome-iron receptor	1.3
429	M37278	R.norvegicus renin gene, exons 1-9.	0.56	2853019	(AF045141) putative serine proteinase [Scirpophaga incertulas]	1.0
430	D28878	Thermus thermophilus polA gene for thermostable DNA polymerase I, complete cds	0.56	3659692	(AF068748) sphingosine kinase [Mus musculus]	0.77
431	Z15027	H.sapiens HLA class III DNA	0.56	1304141	(D43758) fibrinogen A-alpha-chain	0.76
432	M14362	Human T-cell surface antigen CD2 (T11) mRNA, complete cds.	0.56	2462979	(Y11915) Tenascin-X [Bos taurus]	0.59
433	Z50801	Z.mays mRNA for chlorophyll a/b-binding protein CP29	0.56	109677	collagen alpha 1(I) chain - mouse >gi\|50487	0.50

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 86.0 KD	
434	Z38114	S.cerevisiae chromosome XIII cosmid 9745	0.56	140372	PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi\|83159\|pir\|\|S19367 hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae)	0.35
435	AF052254	Escherichia coli DNA gyrase A (gyrA) gene, partial cds	0.56	2724126	(AF038535) synaptotagmin VII [Homo sapiens]	0.12
436	AF080649	Tegula pulligo 12S small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.56	3913223	CYCLIN-DEPENDENT KINASE INHIBITOR 1 p21/WAF1 [Felis catus]	0.11
437	AJ005690	Danio rerio mRNA for protein tyrosine kinase	0.56	2623830	(AF030962) unknown [Schistosoma mansoni]	7e-06
438	U31202	Human noggin (NOGGIN) gene, complete cds.	0.56	3875475	(Z78411) F02D8.3 [Caenorhabditis elegans]	1e-06
439	X51695	Ovis sp. trichohyalin mRNA, partial	0.56	3386622	(AC004665) unknown protein [Arabidopsis thaliana]	1e-10
440	U28938	Rattus norvegicus protein tyrosine phosphatase D30 mRNA, complete cds	0.56	3293547	(AF072709) putative oxidoreductase [Streptomyces lividans]	1e-14
441	AE001171	Borrelia burgdorferi (section 57 of 70) of the complete genome	0.56	2315521	(AF016452) similar to the beta transducin family	4e-16
442	AF036685	Caenorhabditis elegans cosmid C05B10	0.56	1519671	(U67951) contains similarity to ATP/GTP-binding site motif (PS:PS00017) [Caenorhabditis elegans]	6e-20
443	X01173	Xenopus laevis vitellogenin gene A1 5' flanking region	0.56	1118102	(U41558) K02B2.3 gene product [Caenorhabditis elegans]	2e-31
444	D10911	Mus musculus DNA for MS2 protein, complete cds	0.55	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
445	D30010	Rice mRNA EN117, partial sequence	0.55	<NONE>	<NONE>	<NONE>
446	U51991	Escherichia coli phosphoprotein phosphatase	0.55	<NONE>	<NONE>	<NONE>
447	M18858	Mouse T cell receptor C-gamma-7.1 mRNA, 3' end.	0.55	<NONE>	<NONE>	<NONE>
448	U95218	Homo sapiens T cell-death associated protein gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
449	M14948	Human R-ras gene, exon 1.	0.55	<NONE>	<NONE>	<NONE>
450	AB002353	Human mRNA for KIAA0355 gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
451	L81689	Homo sapiens (subclone 1_d6 from P1 H54) DNA sequence	0.55	<NONE>	<NONE>	<NONE>
452	M68955	Human myristoylated alanine-rich C-kinase substrate (MACS) gene, 5' end.	0.55	3322710	(AE001220) V-type ATPase, subunit B (atpB-1) [Treponema pallidum]	5.0
453	X62953	R.norvegicus mRNA (pJG116) with repetitive elements	0.55	1076802	extensin-like protein - maize >gi\|600118 mays]	5.0
454	L34630	Synechocystis sp. mntABC transporter system: periplasmic-binding protein (mntC), complete cds; (mntA) gene, complete cds; membrane protein (mntB) gene, complete cds.	0.55	2117632	hydrogen dehydrogenase (EC 1.12.1.2) - Clostridium acetobutylicum >gi\|557064 (U15277) hydrogenase I [Clostridium acetobutylicum]	5.0
455	U43521	Plasmodium berghei merozoite surface protein-1 gene, complete cds	0.55	127654	MYOGLOBIN	4.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
456	Z64937	H.sapiens CpG DNA, clone 17g7, reverse read cpg17g7.rt1a .	0.55	417298	MFS18 PROTEIN PRECURSOR	3.8
457	U10914	Macaca mulatta clone irh83 T-cell receptor alpha chain mRNA, partial cds.	0.55	310406	(L09212) tat protein [Simian immunodeficiency virus] virus]	3.8
458	AF022838	Homo sapiens multidrug resistance protein	0.55	1585251	traB gene [Amycolatopsis methanolica]	2.8
459	M35603	Mouse Hox-3.1 gene and Hox-3.2-Hox-3.1 intergenic region.	0.55	818849	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]	2.0
460	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi\|74386\|pir\|\|WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
461	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi\|74386\|pir\|\|WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
462	U59736	Human transcription factor (NFATc.b) mRNA, complete cds	0.55	3327144	(AB014565) KIAA0665 protein [Homo sapiens]	0.096
463	U34860	Saccharomyces cerevisiae origin recognition complex large subunit (ORC1) gene, complete cds	0.55	140372	HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi\|83159\|pir\|\|S19367 hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae)	0.017
464	AF012341	Homo sapiens glutaryl-CoA dehydrogenase (GCDH) gene, exons 6, 7, 8, 9, and 10	0.55	1166611	(U46674) coded for by C. elegans cDNA yk27d9.5; coded for by C. elegans cDNA yk27d9.3; short region of weak homology to drosophilia suppressor of sable protein	0.008

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 isolate Q98-				
465	AF004891	CxA from Kenya, envelope glycoprotein C2V3 region (env) gene, partial cds	0.54	<NONE>	<NONE>	<NONE>
466	Y10159	D.discoideum racGAP gene	0.54	<NONE>	<NONE>	<NONE>
467	AB001895	Homo sapiens mRNA for B120, complete cds	0.54	<NONE>	<NONE>	<NONE>
468	X12357	Bovine gene for aspartyl protease NM1 exons 3 and 4 > :: lcl\|X12357 Bovine aspartyl protease NM1 gene, exons 3 and 4.	0.54	<NONE>	<NONE>	<NONE>
469	AE001151	Borrelia burgdorferi (section 37 of 70) of the complete genome	0.54	<NONE>	<NONE>	<NONE>
470	X92052	H.sapiens mRNA for T cell receptor alpha chain	0.54	<NONE>	<NONE>	<NONE>
471	U00938	Mus musculus ileal lipid-binding protein gene, complete cds	0.54	1009712	(U27698) calreticulin [Arabidopsis thaliana]	4.9
472	X68367	M.thermoformicicum complete plasmid pFZ1 DNA	0.54	125272	CASEIN KINASE II, ALPHA CHAIN (CK II) >gi\|419938\|pir\|\|A43297 casein kinase II (EC 2.7.1.-) alpha chain - Theileria parva >gi\|161871 (M92084) casein kinase II alpha subunit [Theileria parva]	4.7
473	Z61098	H.sapiens CpG DNA, clone 44c4, reverse read cpg44c4.rt1a .	0.54	4191274	(AJ131094) Xvent-1B protein [Xenopus laevis]	3.7
474	M63962	Human gastric H,K-ATPase catalytic subunit gene, complete cds.	0.54	3881648	(Z70757) similar to serine protease inhibitor [Caenorhabditis elegans]	3.7
475	X86019	H.sapiens mRNA for PRPL-2 protein	0.54	1648828	(D87963) ETF-related factor-1 (ETFR-1)	2.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		S.glaucescens genes				
476	X89010	strU, strX, strV and strW for 5'-hydroxystreptomycin pruduction and transport polypeptides	0.54	3550345	(AF084524) cellular repressor of E1A-stimulated genes CREG [Mus musculus]	0.25
477	AB007836	Homo sapiens mRNA for Hic-5, partial cds	0.54	1097213	ORF 1 [Streptomyces lavendulae]	0.15
478	U32622	Comamonas testosteroni TsaR (tsaR), toluenesulfonate methyl-monooxygenase oxygenase component component (tsaB), toluenesulfonate zinc-indepedent alcohol dehydrogenase...	0.54	3875351	(Z96047) DY3.6 [Caenorhabditis elegans]	0.006
479	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
480	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
481	Z33072	M.capricolum DNA for CONTIG MC097	0.53	<NONE>	<NONE>	<NONE>
482	U45975	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds.	0.53	<NONE>	<NONE>	<NONE>
483	Z71324	S.cerevisiae chromosome XIV reading frame ORF YNL048w	0.53	2135586	M130 antigen (cytosolic variant 1) - human	2.1
484	L32090	Listeria monocytogenes secA gene, complete cds.	0.53	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.70

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
485	D86423	Mus musculus mRNA for HGT keratin, partial cds	0.53	1235974	(X96713) collagen [Globodera pallida]	0.41
486	Y15969	Mus musculus V kappa 21-6 gene, partial	0.52	<NONE>	<NONE>	<NONE>
487	M27480	Mus musculus (clone 3F9) transcribed germline T cell receptor gamma chain (Tcr-g) mRNA, VJ4 C4 region.	0.52	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	4.6
488	D87004	Human (lambda) DNA for immunogloblin light chain	0.52	1766073	(U37272) winged helix protein CWH-1 [Gallus gallus]	3.5
489	Z99704	Human DNA sequence from cosmid E75B8 on chromosome 22, complete sequence [Homo sapiens]	0.51	<NONE>	<NONE>	<NONE>
490	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
491	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.50	<NONE>	<NONE>	<NONE>
492	M14602	Human myoglobin gene, exon 2.	0.49	478384	helicase homolog g10L protein - African swine fever virus >gi\|414091 (X72951) G10L 125 KDa protein	7.0
493	D87075	Human mRNA for KIAA0238 gene, partial cds	0.24	1938429	(U97002) similar to Schizosaccharomyces pombe 4-nitrophenylphosphatase (PNPPASE) (SP:Q00472, NID:g5004) [Caenorhabditis elegans]	2.5
494	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.23	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		N.crassa				
495	J05254	mitochondrial small (19S) rRNA and Cys-tRNA.	0.23	192150	(L05670) clustrin [Mus musculus]	5.1
496	X16399	Gene for glutamate dehydrogenase (EC 1.4.1.4), put. bacterial origin	0.23	790933	(L07867) invariant surface glycoprotein [Trypanosoma brucei]	0.030
497	AE001251	Treponema pallidum section 67 of 87 of the complete genome	0.22	<NONE>	<NONE>	<NONE>
498	AF026919	Homo sapiens amyloid lambda light chain variable region mRNA, partial cds	0.21	<NONE>	<NONE>	<NONE>
499	Z27247	D.melanogaster mRNA for defensin	0.21	<NONE>	<NONE>	<NONE>
500	Y15608	Candida albicans UBI3 gene	0.21	<NONE>	<NONE>	<NONE>
501	V00598	Human beta-tubulin pseudogene.	0.21	<NONE>	<NONE>	<NONE>
502	X79426	A.thaliana microsatellite [repeated motif (gat)7]	0.21	<NONE>	<NONE>	<NONE>
503	X75772	A.caerulescens mitochondrial genes for cytochrome b and NADH dehydrogenase 5	0.21	139626	PROTEIN T1 PRECURSOR	7.8
504	AF028736	Serratia marcescens site specific recombinase	0.21	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.6
505	X97545	S.cerevisiae OST5 gene	0.21	2275631	(AF014940) No definition line found [Caenorhabditis elegans]	2.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
506	M24543	Human prostate-specific antigen (PA) gene, complete cds.	0.21	1938527	(U97012) C04E6.2 gene product [Caenorhabditis elegans]	2.7
507	M62470	Mouse thrombospondin (THBS1) gene, complete cds.	0.21	548563	RNA REPLICASE POLYPROTEIN 2.7.7.48) - Erysimum latent virus >gi\|3892232 (AF098523) replicase protein [Erysimum latent virus]	2.1
508	Y13544	Homo sapiens cosmid C1	0.21	1235710	(L40584) polyprotein [Infectious pancreatic necrosis virus]	2.0
509	M24193	Chicken MHC B complex protein (C12-3) mRNA, complete cds.	0.21	3600102	(AF090441) extracellular reelin [Gallus gallus]	0.52
510	X97161	H.sapiens TFE3 gene, exon 4,5 & 6	0.21	854065	(X83413) U88 [Human herpesvirus 6]	0.30
511	X67649	R.norvegicus DNA sequence for LFB1/HNF1 promoter	0.21	3913114	TRANSCRIPTION FACTOR COUP 2 COUP-TFII - chicken >gi\|392817 (U00697) orphan receptor COUP-TFII [Gallus gallus]	0.004
512	U63807	Fugu rubripes growth hormone (GH) gene, complete cds	0.21	3510505	(AF030881) pol polyprotein [Fugu rubripes]	3e-04
513	Z95636	H.sapiens mRNA for laminin alpha 5 chain	0.21	400350	NAM7 PROTEIN (NONSENSE MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1) factor NAM7 - yeast (Saccharomyces cerevisiae) >gi\|4023	1e-07
514	U91907	Mirounga leonina major histocompatibility complex class II (DQA) gene, partial cds	0.20	<NONE>	<NONE>	<NONE>
515	Z35758	Transmissible gastroenteritis virus TFI virion protein genes	0.20	<NONE>	<NONE>	<NONE>
516	X00334	Drosophila virilis simple DNA sequence (pDv-19)	0.20	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
517	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.20	<NONE>	<NONE>	<NONE>
518	D78515	Mus musculus rae28 gene, exon 1 and 5'flanking region	0.20	<NONE>	<NONE>	<NONE>
519	M62975	Drosophila melanogaster RNA polymerase II second largest subunit upstream (DmRP 140) gene, exons 1-4.	0.20	<NONE>	<NONE>	<NONE>
520	M27260	Chicken 78-kD glucose-regulated protein, complete cds.	0.20	<NONE>	<NONE>	<NONE>
521	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
522	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
523	U04636	Human cyclooxygenase-2 (hCox-2) gene, complete cds.	0.20	<NONE>	<NONE>	<NONE>
524	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.20	<NONE>	<NONE>	<NONE>
525	AF043514	Mus musculus phosphomannomutase (Pmm2) mRNA, complete cds	0.20	3025006	HYPOTHETICAL 15.5 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION >gi\|1787009 (AE000181) orf, hypothetical protein [Escherichia coli]	9.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
526	U23144	Xenopus laevis FTZ-F1-related nuclear orphan receptor variant (xFF1rAshort) mRNA, complete cds.	0.20	3184402	(AB014477) period protein [Chymomyza costata]	9.6
527	U14621	Paracentrotus lividus Pax-6 (suPax-6) mRNA, complete cds.	0.20	465894	PROBABLE MICROSOMAL SIGNAL PEPTIDASE 23 KD SUBUNIT (SPC22/23) >gi\|630688\|pir\|\|S44854 K12H4.4 protein - Caenorhabditis elegans >gi\|289708 (L14331) homology with signal peptidase; coded for by C. elegans cDNAs GenBank: M79661, M79662 and M79663; putative	7.7
528	AF030511	Actinobacillus pleuropneumoniae MRP ATPase homolog (mrp) gene, partial cds; ApxIVA var3 (apxIVA) gene, complete cds; and beta-galactosidase (lacZ) gene, partial cds	0.20	1175966	HYPOTHETICAL 45.3 KD PROTEIN IN THI5 5'REGION >gi\|1084720\|pir\|\|S56193 probable membrane protein YFL062w - yeast (Saccharomyces cerevisiae)	7.2
529	AF070581	Homo sapiens clone 24540 mRNA sequence	0.20	542394	glyoxal oxidase (EC 1.2.3.-) precursor - basidiomycete (Phanerochaete chrysosporium) >gi\|1050302	5.8
530	X75437	T.maritima pgK gene for 3-phosphoglycerate kinase	0.20	825648	(Z34531) coproporphyrinogen oxidase [Homo sapiens]	5.8
531	U32686	Haemophilus influenzae Rd section 1 of 163 of the complete genome	0.20	3309593	(AF072878) ciliary outer arm dynein beta heavy chain	5.6
532	Z28081	S.cerevisiae chromosome XI reading frame ORF YKL081w	0.20	2507201	CARBON CATABOLITE DEREPRESSING PROTEIN KINASE >gi\|1469803 (L78129) serine/threonine kinase [Candida albicans]	5.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Hordeum vulgare				
533	AF022725	limit dextrinase (HvLD99) gene, complete cds	0.20	3139154	(AF064077) adrenocorticotropic hormone receptor [Sus scrofa]	4.3
534	AL021726	Drosophila melanogaster cosmid 171E4	0.20	3885334	(AC005623) putative argonaute protein [Arabidopsis thaliana]	2.6
535	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.20	4008334	(Z92824) B0413.4 [Caenorhabditis elegans]	1.5
536	Z46606	H.sapiens HLTF gene for helicase-like transcription factor	0.20	132946	60S RIBOSOMAL PROTEIN L30B (RP29) cytosolic - yeast (Saccharomyces cerevisiae) >gi\|171821 not determined) [Saccharomyces cerevisiae] >gi\|1045254 cerevisiae] >gi\|1323250\|gnl\|PID\|e243708 (Z72933) ORF YGR148c [Saccharomyces cerevisiae]	1.5
537	X87193	H.sapiens mRNA for 2.19 gene	0.20	139820	DNA-REPAIR PROTEIN XRCC1	1.5
538	L77965	Clostridium perfringens C beta 2 toxin gene, complete cds	0.20	1175950	HYPOTHETICAL 33.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION >gi\|1084703\|pir\|\|S56211 probable membrane protein YFL044c - yeast (Saccharomyces cerevisiae) >gi\|836711\|gnl\|PID\|d1009835 (D50617) YFL044C	1.4
539	M15938	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 18.	0.20	2133082	regulatory protein MSR1 - yeast	1.1
540	AJ003220	Solanum tuberosum mRNA for extensin-like protein, partial	0.20	2496932	HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III >gi\|726413 (U23177) C56G2.1 gene product [Caenorhabditis elegans]	1.1
541	X98108	A.thaliana psbP gene	0.20	119227	EPIDERMAL GROWTH FACTOR PRECURSOR precursor - mouse >gi\|309210 (J00380) prepro-egf [Mus musculus]	0.49

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
542	AB011179	Homo sapiens mRNA for KIAA0607 protein, partial cds	0.20	2143753	gene VGF protein - rat >gi\|205690 (M60525) nerve growth factor inducible protein [Rattus norvegicus] >gi\|205701 (M60522) nerve growth factor-inducible protein [Rattus norvegicus] >gi\|207651	0.39
543	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.20	629557	RNA-binding protein rnpD - Arabidopsis thaliana (fragment) >gi\|510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.38
544	AB008374	Oncorhynchus mykiss mRNA for alpha 3 type I collagen, partial cds	0.20	1082610	muf1 protein - human >gi\|762953 (X86018) muf1 [Homo sapiens]	0.37
545	U09809	Limulus polyphemus arginine kinase mRNA, complete cds.	0.20	3882016	(AJ012650) CP [Papaya ringspot virus]	0.37
546	AB020671	Homo sapiens mRNA for KIAA0864 protein, partial cds	0.20	2674350	(U93121) M-phase phosphoprotein-1 [Homo sapiens]	0.18
547	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi\|3258651 elegans]	0.043
548	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi\|3258651 elegans]	0.042

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cdk5r=cyclin-				
549	S82819	dependent kinase 5 regulatory subunit p35 [mice, brain, 129/SvJ, C57BL/6, Genomic/mRNA, 5528 nt]	0.20	3413870	(AB007923) KIAA0454 protein [Homo sapiens]	0.020
550	D31792	Streptomyces griseus DNA for serine/threonine protein kinases, complete cds	0.20	861405	(U29154) T07F12.2 gene product [Caenorhabditis elegans]	0.019
551	U97499	Homo sapiens butyrophilin (BT3.2) gene, exons 5-10, and complete cds	0.20	2773341	(AF040954) putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]	0.008
552	U31463	Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, complete cds.	0.20	3880111	(Z81130) predicted using Genefinder	0.002
553	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.20	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	4e-04
554	X57310	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L-cysteinyl-D-valine synthetase and isopenicillin N synthase	0.20	1723511	PUTATIVE ENDONUCLEASE C1F12.06C yeast (Schizosaccharomyces pombe) >gi\|1217980 (Z69944) unknown [Schizosaccharomyces pombe]	4e-09
555	X62386	S.epidermidis genes epiY', epiY, epiA, epiB, epiC, epiD, epiQ, epiP	0.20	3874927	(Z73424) C44B9.1 [Caenorhabditis elegans]	3e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z80220) similar to nucleotide	
556	X59000	Epizootic haemorrhagic disease virus gene segment 6 for NS1	0.20	3879755	binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST EMBL:M89054 comes from this gene; cDNA EST EMBL:D26713 comes from this gene; cDNA EST EMBL:D26718 comes from this gene; cDNA...	8e-16
557	M98776	Human keratin 1 gene, complete cds	0.20	1086900	(U41278) contains similarity to G beta repeats	2e-30
558	AF011446	Mus musculus granzyme K gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
559	AF074708	Macaca mulatta clone MMU1.5 FRG1-like pseudogene, exons 7 and 8, partial sequence	0.19	<NONE>	<NONE>	<NONE>
560	X13287	Medicago sativa nodulin-25 gene	0.19	<NONE>	<NONE>	<NONE>
561	Z49509	S.cerevisiae chromosome X reading frame ORF YJR009c	0.19	<NONE>	<NONE>	<NONE>
562	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.19	<NONE>	<NONE>	<NONE>
563	D29644	Streptococcus salivarius DNA for dextranase	0.19	<NONE>	<NONE>	<NONE>
564	AE001461	Helicobacter pylori, strain J99 section 22 of 132 of the complete genome	0.19	<NONE>	<NONE>	<NONE>
565	L38559	Homo sapiens galactocerebrosidase (GALC) gene, exon 17.	0.19	<NONE>	<NONE>	<NONE>
566	Z82628	R.prowazekii genomic DNA fragment (clone A405F)	0.19	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
567	U25641	Tetrahymena thermophila telomerase component p80 mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
568	AB002343	Human mRNA for KIAA0345 gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
569	D10064	Erwinia carotovora gene for pectate lyase III, complete cds	0.19	<NONE>	<NONE>	<NONE>
570	U31734	Homo sapiens clone MF118 A4A10 hypoxanthine phosphoribosyltransferase (hprt) 130 kb deletion mutant mRNA, partial cds, contains human Alu element	0.19	<NONE>	<NONE>	<NONE>
571	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	0.19	<NONE>	<NONE>	<NONE>
572	M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds.	0.19	<NONE>	<NONE>	<NONE>
573	S67478	(GC*IS)=vitamin D-binding protein/group specific component [human, peripheral blood leukocytes, Genomic, 794 nt, segment 4 of 9]	0.19	<NONE>	<NONE>	<NONE>
574	X99075	H.sapiens NRGN gene, exon 1	0.19	<NONE>	<NONE>	<NONE>
575	AF044775	Homo sapiens breakpoint cluster region BCRder14 sequence	0.19	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for				
576	AB002333	KIAA0335 gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
577	U53566	Macaca mulatta pit-1/GHF-1 transcription factor mRNA, complete cds	0.19	1078068	probable membrane protein YLR311c - yeast	9.2
578	U73664	Human t(11;14)(q13;q32) breakpoint junction sequence	0.19	116734	COAT PROTEIN (CAPSID PROTEIN) virus >gi\|58901 (X62133) CyMV coat protein gene product	8.8
579	AF004054	Heterophyllaea pustulata rps16 gene, chloroplast gene, partial intron sequence	0.19	1928991	(U92815) heat shock protein 70 precursor [Citrullus lanatus]	8.7
580	Z27081	Caenorhabditis elegans cosmid M01A8, complete sequence [Caenorhabditis elegans]	0.19	2496247	HYPOTHETICAL ATP-BINDING PROTEIN MJ0625 >gi\|2128413\|pir\|\|A64378 hypothetical protein MJ0625 - Methanococcus jannaschii >gi\|1591336 (U67510) M. jannaschii predicted coding region MJ0625	8.6
581	Z74145	S.cerevisiae chromosome IV reading frame ORF YDL097c	0.19	1174425	TYROSINE-PROTEIN KINASE SPK-1	6.7
582	D38547	Small round structured virus genomic RNA, 3'terminal sequence containing ORF2 and ORF3	0.19	971318	(Z48053) putative protein [Bovine herpesvirus 1]	5.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
583	D88000	~~Ralstonia eutropha DNA 16S ribosomal~~ RNA > :: dbj\|D88002\|D88002 Ralstonia eutropha DNA for 16S ribosomal RNA > :: dbj\|D88003\|D88003 Ralstonia eutropha DNA for 16S ribosomal RNA > :: dbj\|D88004\|D88004 Ralstonia eutropha DNA for 16S ribosomal RNA	0.19	3800952	(AF100657) No definition line found [Caenorhabditis elegans]	5.1
584	U67462	Methanococcus jannaschii section 4 of 150 of the complete genome	0.19	3183617	(AJ005586) MYB-related transcription factor [Antirrhinum majus]	4.0
585	L23906	Gallus domesticus microsatellite DNA marker.	0.19	1947094	(U93074) voltage-gated sodium channel homolog BdNa1	3.9
586	AE001462	Helicobacter pylori, strain J99 section 23 of 132 of the complete genome	0.19	1730177	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) ISOMERASE) (PHI) >gi\|2118333\|pir\|\|I48073 glucose phosphate isomerase - Chinese hamster >gi\|987046 griseus]	3.9
587	M19460	P.putida catBC operon encoding cis,cis-muconate lactonizing enzyme I and muconolactone isomerase genes, complete cds.	0.19	3873843	(Z82256) cDNA EST yk251g7.3 comes from this gene; cDNA EST yk251g7.5 comes from this gene; cDNA EST EMBL:D68223 comes from this gene; cDNA EST EMBL:C12737 comes from this gene; cDNA EST yk389c8.5 comes from this gene; cDNA E...	3.9
588	U22349	Tetrahymena australis telomerase RNA gene, complete sequence	0.19	4105782	(AF049922) PGP169-12 [Petunia x hybrida]	3.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
589	L27745	Homo sapiens voltage operated calcium channel, alpha-1 subunit mRNA, complete cds.	0.19	3763926	(AC004450) unknown protein [Arabidopsis thaliana]	3.0
590	AF049588	Canis familiaris synapsin I gene, partial cds	0.19	4104931	(AF042196) auxin response factor 8 [Arabidopsis thaliana]	3.0
591	X06627	Staphylococcus aureus plasmid pS194 sequence	0.19	137927	PRE-NECK APPENDAGE PROTEIN (LATE PROTEIN GP12) >gi\|75856\|pir\|\|WMBP22 gene 12 protein - phage phi-29 >gi\|215330 (M14782) pre-neck appendage protein [Bacteriophage phi-29] >gi\|225367\|prf\|\|1301270G gene 12 [Bacteriophage phi-29]	2.3
592	X61597	M.musculus gene for kallikrein-binding protein	0.19	2982874	(AE000675) cobalamin synthesis related protein CobW	1.7
593	AF016242	Dictyostelium discoideum protein synthesis elongation factor 1-alpha (tef2) gene, partial cds	0.19	133659	PUTATIVE RNA-DIRECTED RNA POLYMERASE	1.4
594	AF004447	Venezuelan equine encephalitis virus strain 1327 polyprotein gene, partial cds > :: gb\|AF004460\|AF004460 Venezuelan equine encephalitis virus strain 1385 polyprotein gene, partial cds	0.19	4096173	(U25968) early embryogenesis protein [Oryza sativa]	1.3
595	J04821	Human elastin (ELN) gene, exon 1, clones HELC-5 and HELC-6.	0.19	1170523	INHIBIN BETA B CHAIN PRECURSOR inhibin precursor - bovine >gi\|563753 (U16241) betaB inhibin/activin precursor [Bos taurus]	1.3
596	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.19	3024881	PROBABLE TRANSPORT PROTEIN CY21C12.11 >gi\|2078066\|gnl\|PID\|e315171 (Z95210) betP	0.83

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					FERREDOXIN-DEPENDENT	
597	M69053	D.melanogaster calcium-activated K+ channel subunit	0.19	1707984	GLUTAMATE SYNTHASE 1 (FD-GOGAT) >gi\|2126524\|pir\|\|S60228 glutamate synthase (ferredoxin) (EC 1.4.7.1) gltB - Synechocystis sp. (PCC 6803) >gi\|515938 (X80485) glutamate synthase	0.80
598	AF076279	Dictyostelium firmibasis plasmid Dfp1, complete plasmid sequence	0.19	453986	(U00008) yejA [Escherichia coli]	0.79
599	D28873	Mouse MCNP gene for C-type natriuretic peptide, complete cds (exon1, exon2)	0.19	2650444	(AE001092) acetyl-CoA synthetase (acs-1) [Archaeoglobus fulgidus]	0.63
600	U06071	Oxytricha nova macronuclear actin II gene, complete cds.	0.19	1584024	complement control protein [Botryllus schlosseri]	0.48
601	L54057	Homo sapiens CLP mRNA, partial cds.	0.19	3036883	(AL022374) putative ABC transporter	0.46
602	X89806	P.lividius cDNA for COLL2alpha gene	0.19	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	0.41
603	AE001104	Archaeoglobus fulgidus section 3 of 172 of the complete genome	0.19	2315192	(Y11739) transcription factor [Homo sapiens]	0.35
604	U54501	Rattus norvegicus microsatellite sequence D0Mco22	0.19	228951	D-MeAsp receptor:ISOTYPE=epsilon3 [Mus musculus]	0.32
605	X74468	Human papillomavirus type 15 genomic DNA	0.19	3695390	(AF096371) contains similarity to Rattus norvegicus cyclin G-associated kinase (SW:P97874) [Arabidopsis thaliana]	0.28
606	U20285	Human Gps1 (GPS1) mRNA, complete cds	0.19	2582659	(AJ002527) glucitol-6-phosphate dehydrogenase [Clostridium beijerinckii]	0.27
607	D49408	Human gene for interleukin 3 receptor alpha subunit, exon 10	0.19	2522368	(AF008596) alpha1,3-fucosyltransferase [Helicobacter pylori]	0.16

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
608	AF041141	Homo sapiens pituitary specific homeodomain protein (PROP1) gene, exon 3 and complete cds	0.19	37403	(X03541) trk gene product (aa 1-641) [Homo sapiens]	0.091
609	L12531	Discopyge ommata Ca2+ channel alpha 1 subunit gene sequence.	0.19	3618274	(AJ223219) hypothetical protein	0.069
610	AF052445	Yellow fever virus clone HONG9 polyprotein gene, complete cds	0.19	1932822	(U15928) KH-domain putative RNA binding protein	0.001
611	Z36946	B.anthracis sap gene encoding S-layer protein	0.19	173241	(L06487) ZIP1 protein [Saccharomyces cerevisiae]	2e-04
612	AF087984	Homo sapiens full length insert cDNA clone YW29A12	0.19	3786014	(AC005499) hypothetical protein [Arabidopsis thaliana]	1e-06
613	AE001010	Archaeoglobus fulgidus section 97 of 172 of the complete genome	0.19	3135493	(AF060248) unknown [Arabidopsis thaliana]	7e-08
614	L08965	Trichosporon cutaneum carbamoyl phosphate synthetase large subunit (argA) gene, partial cds.	0.19	1086901	(U41278) F33G12.3 gene product [Caenorhabditis elegans]	2e-08
615	M91466	Rattus norvegicus A2b-adenosine receptor mRNA, complete cds.	0.19	2984320	(AE000773) acetoin utilization protein [Aquifex aeolicus]	6e-09
616	X95971	S.lividans groEL2 gene	0.19	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	7e-10
617	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete cds.	0.19	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	3e-14

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U97016) similar to drosophila	
618	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete cds.	0.19	1938549	Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	9e-15
619	Z68327	Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.	0.19	3875774	(Z68257) cDNA EST EMBL:D32434 comes from this gene; cDNA EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ... >gi\|3878710\|gnl\|PID\|e1348373 EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ...	6e-15
620	U66525	Dictyostelium discoideum ORFveg114 mRNA, complete cds	0.19	3540281	(AF056116) All-1 related protein [Fugu rubripes]	2e-17
621	U25830	Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds	0.19	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	1e-18
622	U89407	Mus musculus strain BALB/c delta-aminolevulinic acid dehydratase (Lv) mRNA, partial cds	0.19	1825764	(U88314) C46H11.11 gene product [Caenorhabditis elegans]	3e-25
623	AF095598	Bison bison athabascae microsatellite BBJ 2	0.18	<NONE>	<NONE>	<NONE>
624	AF064260	Strongylocentrotus purpuratus SRC8 mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
625	U69533	Arabidopsis thaliana AtKAP alpha mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
626	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.18	<NONE>	<NONE>	<NONE>
627	M24571	Dictyostelium discoideum tRNA-Glu-GAA gene, clone yGluGAA7.	0.18	<NONE>	<NONE>	<NONE>
628	X59772	D.melanogaster ovo gene required for female germ line development	0.18	<NONE>	<NONE>	<NONE>
629	AL010209	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-104, complete sequence	0.18	<NONE>	<NONE>	<NONE>
630	U67575	Methanococcus jannaschii section 117 of 150 of the complete genome	0.18	111839	inositol 1,4,5-triphosphate receptor 2 - rat	8.5
631	U28730	Caenorhabditis elegans cosmid K10B2	0.18	1787604	(AE000232) orf, hypothetical protein [Escherichia coli]	8.3
632	X99798	L.lactis pepF1 & pepF2 genes	0.18	3406624	(AF079110) glycosomal malate dehydrogenase [Trypanosoma brucei]	8.1
633	AF025306	Danio rerio band 4.1-like protein 4 (nbl4) mRNA, complete cds	0.18	465445	PROBABLE NUCLEAR ANTIGEN herpesvirus 1 (strain Kaplan) >gi\|334072 (M34651) ORF-3 protein [Pseudorabies virus]	7.9
634	AF059251	Mus musculus lipoxygenase (alox) mRNA, complete cds	0.18	1655667	(Z81368) hypothetical protein Rv2393	6.6
635	Z22605	G.domesticus CTCF protein mRNA.	0.18	481864	3-methyl-2-oxobutanoate dehydrogenase	6.6
636	AB011086	Homo sapiens mRNA for KIAA0514 protein, complete cds	0.18	3874158	(Z81464) predicted using Genefinder	6.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
637	Z78536	elegans cosmid C07A4, complete sequence [Caenorhabditis elegans]	0.18	3702121	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]	6.4
638	U67530	Methanococcus jannaschii section 72 of 150 of the complete genome	0.18	3877946	(Z81094) Weak similarity to 65 KDA heat shock protein (TR:G602231); cDNA EST EMBL:D71705 comes from this gene; cDNA EST EMBL:D74382 comes from this gene [Caenorhabditis elegans]	6.3
639	M63781	Influenza A/Duck/England/1/62 (H4N6) nucleoprotein mRNA, complete cds.	0.18	3873663	(Z69634) cDNA EST EMBL:D71510 comes from this gene; cDNA EST EMBL:C08449 comes from this gene; cDNA EST yk266b12.3 comes from this gene; cDNA EST yk266b12.5 comes from this gene; cDNA EST yk461h7.3 comes from this gene; cDNA...	6.2
640	M73781	Oryctolagus cuniculus integrin beta-8 subunit mRNA, complete cds. > :: gb\|I44828\|I44828 Sequence 3 from patent US 5635601	0.18	1362129	major allergen OLE17 - common olive	5.8
641	X67219	D.melanogaster Rop gene	0.18	3449286	(AB011527) MEGF1 [Rattus norvegicus]	4.8
642	AF106941	Homo sapiens beta-arrestin 2 mRNA, complete cds	0.18	548353	[PROTEIN-PII] URIDYLYLTRANSFERASE vinelandii >gi\|39257 (X59610) uridylyl transferase	3.7
643	AF052602	Danio rerio huntingtin (HD) mRNA, complete cds	0.18	241058	potential IGF binding protein [chickens, Peptide Partial, 77 aa, segment 2 of 3]	3.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z68314) predicted using	
644	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.18	3875570	Genefinder; cDNA EST EMBL:M75775 comes from this gene; cDNA EST EMBL:M89255 comes from this gene; cDNA EST EMBL:M89127 comes from this gene; cDNA EST EMBL:T00141 comes from this gene; cDNA EST EMBL:T...	2.1
645	AF096883	HIV-1 isolate patient 3 country USA pol polyprotein (pol) gene, partial cds	0.18	3250696	(AL024486) putative protein	1.7
646	L39928	Pyrocoelia miyako (clone pB-PmL41) luciferase mRNA, complete cds	0.18	2914702	(AC003974) unknown protein [Arabidopsis thaliana]	0.73
647	M17082	Human carcinoembryonic nonspecific crossreacting antigen (CEA; NCA) gene, exons 1 and 2.	0.18	1351833	REGULATORY PROTEIN ABAA	0.72
648	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.18	629557	RNA-binding protein rnpD - Arabidopsis thaliana (fragment) >gi\|510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.41
649	AF011908	Mus musculus apoptosis associated tyrosine kinase (AATYK) mRNA, complete cds	0.18	330442	(K03332) nuclear antigen 2 [Epstein-Barr virus]	5e-04
650	U04004	Simian immunodeficiency virus SIVagmVER-2 envelope protein gene, partial cds.	0.18	135102	ASPARTYL-TRNA SYNTHETASE aspartate--tRNA ligase (EC 6.1.1.12) - Escherichia coli coli] >gi\|1736513\|gnl\|PID\|d1016401 (D90829) Aspartate--tRNA ligase (EC 6.1.1.12) [Escherichia coli]	6e-11
651	U88155	Xenopus laevis RanGTPase activating protein	0.18	995714	(X91258) pid:e198503 [Saccharomyces cerevisiae]	2e-13

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z66511) similar to ribokinase;	
652	Z18921	B.oleracea gene for S-receptor kinase-like protein	0.18	3875535	cDNA EST EMBL:D69553 comes from this gene; cDNA EST EMBL:D65938 comes from this gene; cDNA EST yk280h9.3 comes from this gene; cDNA EST yk280h9.5 comes from this gene; cDNA EST yk223d11.3 come...	1e-19
653	M60650	S.cerevisiae STA2 gene, complete cds.	0.16	<NONE>	<NONE>	<NONE>
654	U80912	Eucalyptus globulus NADP-isocitrate dehydrogenase (EgICDH) mRNA, complete cds	0.16	3766172	(AF057298) ornithine decarboxylase antizyme 2 [Mus musculus]	4.2
655	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.16	76749	hypothetical protein 4 - fowl adenovirus 1	4.0
656	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.16	3044086	(AF055904) unknown [Myxococcus xanthus]	0.60
657	AF030231	Glycine max sucrose synthase (SS) mRNA, complete cds	0.078	<NONE>	<NONE>	<NONE>
658	M19183	Woodchuck hepatitis virus (WHV), complete genome, clone WHV 59.	0.072	1076190	cell wall glycoprotein, 75K, precursor - diatom (Cylindrotheca fusiformis) >gi\|515363 (X80394) P75K gene product [Cylindrotheca fusiformis]	6.3
659	U31557	Ovine adenovirus IVa2 protein gene, DNA polymerase gene, terminal protein gene and 52,55 kDa protein gene, partial cds	0.072	3511143	(AF061244) unknown [Agrocybe aegerita]	6.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
660	AL021491	elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.070	<NONE>	<NONE>	<NONE>
661	M33874	X.laevis Xotch protein mRNA, complete cds.	0.070	1654096	(Y09076) RAD3 [Schizosaccharomyces pombe]	0.23
662	AB012725	Mus musculus ZAN75 mRNA for zinc finger protein, complete cds	0.069	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	2.0
663	AL021491	Caenorhabditis elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.068	<NONE>	<NONE>	<NONE>
664	Z60318	H.sapiens CpG DNA, clone 1e1, reverse read cpg1e1.r1a .	0.068	1280134	(U55376) F16H11.2 gene product [Caenorhabditis elegans]	2.6
665	Z35973	S.cerevisiae chromosome II reading frame ORF YBR104w	0.068	2493000	PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR EMBL:Z14816 comes from this gene; cDNA EST EMBL:Z14946 comes from this gene; cDNA EST EMBL:D69746 comes from this gene; cDNA EST yk219b6.3 comes from this gene; cDNA ES...	0.68
666	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames	0.068	1235974	(X96713) collagen [Globodera pallida]	4e-04
667	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.068	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	1e-59

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
668	M34161	Rat tachykinin (PPT) gene, exons 5 and 6.	0.067	<NONE>	<NONE>	<NONE>
669	L03811	Aspergillus niger zinc finger protein (creA) gene, complete cds.	0.067	<NONE>	<NONE>	<NONE>
670	M64983	Human fibrinogen beta chain gene, complete mRNA. > gb\|I47706\|I47706 Sequence 3 from patent US 5639940	0.067	<NONE>	<NONE>	<NONE>
671	AF014051	Nicotiana tabacum Mg chelatase subunit (ChlH) mRNA, partial cds	0.067	<NONE>	<NONE>	<NONE>
672	Y07540	H.sapiens sil gene	0.067	92331	glycoprotein GP330, renal - rat (fragments)	7.5
673	AJ000347	Rattus norvegicus mRNA for 3'(2'),5'-bisphosphate nucleotidase	0.067	129238	25 KD OOKINETE SURFACE ANTIGEN PRECURSOR (PRS25) >gi\|320962\|pir\|\|A44966 25k ookinete surface antigen precursor - Plasmodium reichenowi reichenowi]	7.4
674	L19979	Squid sodium channel mRNA, complete cds.	0.067	2128473	hypothetical protein MJ0750 - Methanococcus jannaschii >gi\|1592304 (U67521) ferredoxin-type protein	1.5
675	X08050	Yeast tRNA-Glu(3) gene and flanking regions	0.067	1334398	(X15081) MURF2 protein (AA 1-348)	0.65
676	X17115	Human mRNA for IgM heavy chain complete sequence	0.067	1731331	HYPOTHETICAL 51.6 KD PROTEIN CY49.14C >gi\|1370241\|gnl\|PID\|e247089 (Z73966) hypothetical protein Rv2075c [Mycobacterium tuberculosis]	0.51
677	AF032871	Homo sapiens uncoupling protein 3 (UCP3) gene, exon 1 and partial exon 2	0.067	112900	ALPHA-2C-1 ADRENERGIC RECEPTOR human >gi\|178194 (J03853) kidney alpha-2-adrenergic receptor [Homo sapiens] >gi\|1628638 (U72648) alpha2-C4-adrenergic receptor [Homo sapiens]	0.50

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DYNAMIN 3 (DYNAMIN,	
678	X05319	Mouse class II MHC E-beta 2 (d) gene exon 3	0.067	585074	TESTICULAR) rat >gi\|391872\|gnl\|PID\|d1003668 (D14076) testicular dynamin [Rattus norvegicus]	3e-04
679	AB006362	Candida albicans CaSLN1 gene, complete cds	0.067	3417296	(AC003007) Unknown gene product (partial) [Homo sapiens]	9e-56
680	AF021236	African horse sickness virus capsid VP3 (L3) mRNA, complete cds	0.066	<NONE>	<NONE>	<NONE>
681	AE001507	Helicobacter pylori, strain J99 section 68 of 132 of the complete genome	0.066	<NONE>	<NONE>	<NONE>
682	AF039717	Caenorhabditis elegans cosmid R13H8	0.066	<NONE>	<NONE>	<NONE>
683	AF029027	Syncerus caffer isolate Queen Elizabeth Mweya 14 mitochondrial DNA control region	0.066	<NONE>	<NONE>	<NONE>
684	AF087967	Homo sapiens full length insert cDNA clone YU51G05	0.066	2982476	(X97203) C1 protein [Beet curly top virus]	9.5
685	J02037	Baboon endogenous virus proviral long terminal repeat DNA.	0.066	972767	(L37868) POU-domain transcription factor [Homo sapiens]	7.3
686	AF000141	Lycopersicon esculentum class I knotted-like homeodomain protein (LeT6) mRNA, complete cds	0.066	3157926	(AC002131) Strong similarity to extensin-like protein gb\|Z34465 from Zea mays. [Arabidopsis thaliana]	5.6
687	AB001746	Bensingtonia sp. OK255 gene for 18S rRNA > :: dbj\|AB001747\|AB001747 Bensingtonia sp. OK259 gene for 18S rRNA	0.066	3859889	(AF070064) cap 'n' collar isoform C [Drosophila melanogaster]	0.38

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Helicobacter pylori,				
688	AE001461	strain J99 section 22 of 132 of the complete genome	0.065	<NONE>	<NONE>	<NONE>
689	M30821	Chicken erythroid transport proteins c1 and c2	0.065	<NONE>	<NONE>	<NONE>
690	AB009802	Homo sapiens gene for osteonidogen, intron 3	0.065	<NONE>	<NONE>	<NONE>
691	AF086062	Homo sapiens full length insert cDNA clone YZ06B11	0.065	<NONE>	<NONE>	<NONE>
692	AB002369	Human mRNA for KIAA0371 gene, complete cds	0.065	2500884	SIGNAL SEQUENCE BINDING PROTEIN binding protein [Synechococcus sp.]	5.5
693	AF086864	Cyclopodia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence > :: gb\|AF086866\|AF086866 Penicillidia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence	0.065	3721684	(AB012957) probable glycosyl transferase [Vibrio cholerae]	5.5
694	L44593	Bacteriophage BK5-T ORF'410, 3' end pf cds, 20 ORFs, repressor protein, and Cro repressor protein genes, complete cds, ORF70' gene, 5' end of cds.	0.065	1172067	PEPTIDASE T (AMINOTRIPEPTIDASE) influenzae Rd]	3.2
695	U80079	Ciona intestinalis MyoD-family protein (CiMDFa) mRNA, complete cds	0.065	4218110	(AL035353) contains EST gb:F15281	2.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
696	AB020718	Homo sapiens mRNA for KIAA0911 protein, complete cds	0.065	1722734	MINOR CAPSID PROTEIN L2 >gi\|1020192 type 23]	1.9
697	AF082137	Zea mays copia-like retrotransposon Stl-14 leader region, partial sequence	0.065	1877501	(U89278) polyhomeotic 2 homolog [Homo sapiens]	1.1
698	X64053	R.norvegicus ZnBP gene for zinc binding protein	0.065	464963	TRYPSIN PRECURSOR	0.36
699	U67065	Mus musculus butyrophilin (BTN) gene, promoter region and complete cds	0.065	2132252	hypothetical protein YPL263c - yeast	3e-10
700	M64862	Rat matrin F/G mRNA, complete cds.	0.065	3420183	(AF041105) organic anion transporter protein 3 [Rattus norvegicus]	4e-19
701	K02205	Yeast (S.cerevisiae) transcriptional activator of amino acid-biosynthetic genes (GCN4) gene, complete cds.	0.064	<NONE>	<NONE>	<NONE>
702	X58282	Maize mRNA for a high mobility group protein	0.064	<NONE>	<NONE>	<NONE>
703	AC001545	Homo sapiens (subclone 1_f3 from P1 H69) DNA sequence	0.064	<NONE>	<NONE>	<NONE>
704	AF023461	Homo sapiens FRA3B region sequence	0.064	<NONE>	<NONE>	<NONE>
705	U50307	Caenorhabditis elegans cosmid F43H9.	0.064	<NONE>	<NONE>	<NONE>
706	U46542	Streptococcus crista HmpA gene, partial cds, putative adhesin/ABC transport system protein (scbA) gene, complete cds	0.064	1209391	(D83659) TPR protein pombe] >gi\|2894282\|gnl\|PID\|e1251103 (AL021838) pre-mrna splicing factor. [Schizosaccharomyces pombe]	9.2
707	X57564	A.rusticana mRNA for neutral peroxidase	0.064	1492037	(U60315) MC094R [Molluscum contagiosum virus subtype 1]	6.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
708	U06986	Human alpha-2-macroglobulin receptor/lipoprotein receptor protein (A2MR/LRP) gene, exons 39-41.	0.064	100800	rab15B protein - wheat >gi\|21853 (X62476) rab protein [Triticum aestivum]	5.3
709	D85773	Human CpG island sequence, clone Q28B8	0.064	2245382	(U88325) suppressor of cytokine signalling-1 [Mus musculus]	5.3
710	L06178	Apis mellifera ligustica complete mitochondrial genome	0.064	3695379	(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]	3.2
711	Y16242	Triticum aestivum mRNA for beta-amylase	0.064	1175958	HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REGION >gi\|1084712\|pir\|\|S56201 probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) >gi\|836701\|gnl\|PID\|d1009825 (D50617) YFL054C	3.1
712	L81779	Homo sapiens (subclone 2_a2 from P1 H25) DNA sequence	0.064	3845169	(AE001391) phosphatase (acid phosphatase family)	0.81
713	X13826	C.reinhardtii psb1 mRNA for OEE1 protein of photosystem II (oxygen-evolving enhancer protein)	0.064	171040	(M94535) ATPase [Saccharomyces cerevisiae] cerevisiae, Peptide, 377 aa] [Saccharomyces cerevisiae]	0.054
714	X06487	H.sapiens mRNA for bcl2-Ig fusion gene	0.064	2429362	(AF020261) proline rich protein [Santalum album]	0.016
715	U79638	Mus musculus cyclin-dependent kinase inhibitor protein (p15(INK4b)) gene, exon 2 and partial cds	0.064	3929221	(AF082557) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]	1e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human T cell				
716	U39099	receptor alpha chain mRNA, partial cds	0.063	<NONE>	<NONE>	<NONE>
717	U39673	Clostridium acetobutylicum KdpC (kdpC) gene, partial cds, sensor histidine kinase homolog (kdpD) and response regulator homolog (kdpE) genes, complete cds	0.063	<NONE>	<NONE>	<NONE>
718	AL022317	Human DNA sequence from clone 140L1 on chromosome 22q13.1-13.31, complete sequence [Homo sapiens]	0.063	1931640	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]	5.2
719	U28972	Spiroplasma citri orfa and orff genes, partial cds, orfb, orfc, and orfe genes and Spiroplasma virus SpV1-derived ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.	0.063	4091939	(AF070704) envelope glycoprotein [Human immunodeficiency virus type 1]	5.2
720	U15159	Mus musculus limk kinase (limk) mRNA, complete cds	0.063	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	5.1
721	AF058416	Homo sapiens lipoprotein receptor-related protein (LRP1), exons 39, 40, and 41	0.063	1788123	(AE000276) orf, hypothetical protein [Escherichia coli]	4.0
722	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.063	2244849	(Z97337) hypothetical protein	4.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Streptococcus			(Z70203) cDNA EST	
723	L29323	pneumoniae methyl transferase gene cluster, complete sequence	0.063	3874022	EMBL:D72339 comes from this gene; cDNA EST EMBL:D75197 comes from this gene [Caenorhabditis elegans]	2.3
724	X72631	H.sapiens mRNA encoding Rev-ErbAalpha > :: emb\|X72632\|HSREV ERB2 H.sapiens mRNA encoding Rev-ErbAalpha (internal fragment)	0.063	3979878	(Z73105) predicted using Genefinder; cDNA EST EMBL:T01277 comes from this gene; cDNA EST EMBL:T01796 comes from this gene; cDNA EST EMBL:D32545 comes from this gene; cDNA EST EMBL:D33060 comes from this gene; cDNA EST EMBL:D...	1.7
725	U17969	Human initiation factor eIF-5A gene, complete cds.	0.063	2429509	(AF025467) contains similarity to drosophila DNA-binding protein K10 (NID:g8148) [Caenorhabditis elegans]	1.4
726	AE001000	Archaeoglobus fulgidus section 107 of 172 of the complete genome	0.063	3462802	(AF082486) nef protein [Human immunodeficiency virus type 1]	0.35
727	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	0.063	1326288	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.093
728	AF109134	Homo sapiens 7-60 mRNA, complete cds	0.063	1083764	proline-rich proteoglycan 2 precursor, parotid - rat >gi\|310200 (L17318) proline-rich proteoglycan [Rattus norvegicus]	0.001
729	D87466	Human mRNA for KIAA0276 gene, partial cds	0.063	2879865	(AL021816) SPBC24E9.03c, unknown, len:251aa [Schizosaccharomyces pombe]	6e-05
730	AB018269	Homo sapiens mRNA for KIAA0726 protein, complete cds	0.063	2995865	(AF053455) tetraspan TM4SF [Homo sapiens]	2e-16
731	D86954	Cricetulus griseus mRNA for Cytochrome P-450 2A14, complete cds	0.063	2496896	HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III >gi\|3874383\|gnl\|PID\|e1344077 type (RING finger) [Caenorhabditis elegans]	1e-22

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
732	AL010232	falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-58, complete sequence	0.062	<NONE>	<NONE>	<NONE>
733	U90714	Mycoplasma gallisepticum haemagglutinin precursor genes, complete cds	0.062	<NONE>	<NONE>	<NONE>
734	AF107044	Homo sapiens clone pCL4 DNA-binding protein SOX21 (SOX21) gene, complete cds	0.062	<NONE>	<NONE>	<NONE>
735	L41729	Caenorhabditis elegans Ro ribonucleoprotein autoantigen mRNA, complete cds	0.062	2983060	(AE000687) putative protein [Aquifex aeolicus]	8.6
736	Z99287	Caenorhabditis elegans cosmid Y7A9D, complete sequence [Caenorhabditis elegans]	0.062	1176542	PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME III >gi\|495684 (U00065) contains EGF-like repeats; highly similar to ZC84.1; 3' exons similar to protein kinase [Caenorhabditis elegans]	5.8
737	AB014514	Homo sapiens mRNA for KIAA0614 protein, partial cds	0.062	4033395	DNA GYRASE SUBUNIT B subunit [Myxococcus xanthus]	3.9
738	L29165	Human germline immunoglobulin light chain variable region (lambda-IIIb subgroup) from IgM rheumatoid factor.	0.062	1914685	(Y12014) RAD23 protein, isoform II	1.3
739	U09364	Schistosoma japonicum Chinese clone pY6 paramyosin mRNA, partial cds.	0.062	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	1.3
740	Y16242	Triticum aestivum mRNA for beta-amylase	0.062	79834	hypothetical protein 1246 (uvrA region) - Micrococcus luteus (fragment)	0.59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Leishmania pifanoi			TROPOMYOSIN 1 (TMI)	
741	M97695	cysteine proteinase (cys2) gene, complete cds.	0.062	1174754	(POLYPEPTIDE 49) >gi\|320989\|pir\|\|A60607 tropomyosin - fluke	0.018
742	U67526	Methanococcus jannaschii section 68 of 150 of the complete genome	0.062	1330345	(U58755) coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	1e-40
743	Z78414	Caenorhabditis elegans cosmid W09D12, complete sequence [Caenorhabditis elegans]	0.061	<NONE>	<NONE>	<NONE>
744	Y13606	Mus musculus gene encoding filensin, exons 6, 7	0.061	2314715	(AE000651) H. pylori predicted coding region HP1527	4.9
745	J04374	Eggplant mosaic virus genome.	0.061	141449	HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556 >gi\|80759\|pir\|\|JQ0431 hypothetical 35.5K protein - Streptomyces fradiae transposon Tn4556	3.8
746	AB022200	Marine obligately oligotrophic bacterium POO-10 DNA for 16S ribosomal RNA, partial sequence	0.061	3983593	(AB000307) transcarboxylase-beta	2.2
747	X54250	Rat mRNA for zinc finger protein AT-BP2, partial cds	0.061	1377886	(L46815) DNA binding protein Rc [Mus musculus]	0.98
748	X69942	M.musculus mRNA of enhancer-trap-locus 1	0.061	2983969	(AE000748) putative protein [Aquifex aeolicus]	0.57
749	AJ223206	Mus musculus mRNA for scrapie responsive protein 1	0.061	4204265	(AC005223) 45643 [Arabidopsis thaliana]	5e-31
750	Y10205	H.sapiens mRNA for CD88 protein	0.060	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
751	U79260	Human clone 23745 mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
752	X07453	Plasmodium falciparum 11-1 gene part 1	0.060	<NONE>	<NONE>	<NONE>
753	U57502	Rattus norvegicus protein tyrosine phosphatase delta gene, catalytic domain, partial cds.	0.060	3452285	(AF044915) polar tube protein PTP55 precursor	0.28
754	X68359	M.fascicularis gene for apolipoprotein C-III	0.060	730843	SHUTTLE CRAFT PROTEIN >gi\|487400	2e-04
755	X51634	Pseudomonas braB gene for branched chain amino acid transport carrier (LIV-II)	0.059	1835622	(U85718) CCML [Pseudomonas putida GB-1]	8.1
756	AF072405	Gossypium hirsutum cotton fiber expressed protein 2 (CFE2) mRNA, complete cds	0.059	423766	alkaline phosphatase, 145K - Synechococcus sp.	4.7
757	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.056	2662481	(AF034859) juvenile hormone resistance protein	3.3
758	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.054	547847	LECTIN PRECURSOR	7.0
759	X61046	Hydra N-COL 2 mRNA for mini-collagen, partial cds	0.053	<NONE>	<NONE>	<NONE>
760	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.052	<NONE>	<NONE>	<NONE>
761	S79843	{random amplified hybridization microsatellite RAHM} [Beta vulgaris=sugar beets, Genomic, 537 nt]	0.025	1730145	GAMETOGENESIS EXPRESSED PROTEIN GEG-154 >gi\|2137331\|pir\|\|I48361 gene GEG-154 protein - mouse >gi\|550123 (X71642) pid:g550123 [Mus musculus]	2e-16

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
762	AB000096	Mouse mRNA for GATA-2 protein, complete cds	0.023	<NONE>	<NONE>	<NONE>
763	Z62366	H.sapiens CpG DNA, clone 67h7, forward read cpg67h7.ft1a .	0.023	3123312	ZINC FINGER PROTEIN 142 (KIAA0236) to Human zinc finger protein(ZNF142) [Homo sapiens]	5.9
764	L11670	Human transmembrane glycoprotein (CD53) gene, exons 2 through 8.	0.023	80636	hypothetical 67K protein - Mycobacterium fortuitum plasmid pAL5000 >gi\|149986 (M60875) ORF2	3.4
765	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.023	3114665	(AF061267) inner membrane component HtxE [Pseudomonas stutzeri]	3.4
766	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.023	683532	(X02155) thyroglobulin [Bos taurus]	1.1
767	U58835	Dissostichus mawsoni preprotrypsin gene, complete cds	0.022	<NONE>	<NONE>	<NONE>
768	AJ009630	Glomus versiforme chitin synthase gene (clone Gvchs3)	0.022	<NONE>	<NONE>	<NONE>
769	J04040	Human glucagon mRNA, complete cds.	0.022	<NONE>	<NONE>	<NONE>
770	X74908	L.esculentum Asr3 gene	0.022	<NONE>	<NONE>	<NONE>
771	L07293	Shigella dysenteriae O-antigen polysaccharide biosynthesis rfbX, O-antigen polymerase (rfc), rhamnosyl tranferase I and II (rfbR and rfbQ) and rfbD genes, complete cds.	0.022	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
772	AF040094	inositol polyphosphate 5-phosphatase II (INPP5P) mRNA, complete cds	0.022	<NONE>	<NONE>	<NONE>
773	X76776	H.sapiens HLA-DMB gene	0.022	<NONE>	<NONE>	<NONE>
774	AE001521	Helicobacter pylori, strain J99 section 82 of 132 of the complete genome	0.022	<NONE>	<NONE>	<NONE>
775	X16004	A.longa rbcL, rpl5, rps8, rpl36, rps14, rps2, trnI,trnF, trnC and rpoB (partial) genes > :: emb\|X75651\|ALRIBP A.longa plastid genes for ribosomal proteins, tRNAs, RNA polymerase subunit beta and rubisco large subunit	0.022	<NONE>	<NONE>	<NONE>
776	Y12707	Lactococcus lactis cremoris plasmid pHW393 DNA, rlladii, mlladii genes	0.022	<NONE>	<NONE>	<NONE>
777	U27118	Arabidopsis thaliana glutamyl-tRNA reductase	0.022	<NONE>	<NONE>	<NONE>
778	Z96622	H.sapiens telomeric DNA sequence, clone 5PTEL002, read 5PTELOO002.seq	0.022	191333	(J05503) carbamoyl-phosphate synthetase (E.C.6.3.5.5)	9.8
779	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.022	1078509	probable membrane protein YDR018c - yeast	9.7
780	Z77952	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA4A3	0.022	4204206	(AB022786) N-acetyl-beta-D-glucosaminidase [Enterobacter sp.]	7.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis				
781	M10217	mitochondrial DNA, complete genome.	0.022	2145763	B2168_C2_205 protein - Mycobacterium leprae	7.3
782	M55147	Pea chloroplast glyceraldehyde-3-phosphate dehydrogenase (Gpb1) gene, complete cds.	0.022	417308	PROBABLE HELICASE MOT1 Mot1p is a probable helicase essential for vegetative growth on rich glucose medium at 30 degree C: Swiss-Prot Accession number P32333; similar to S. cerevisiae RAD26 gene product: Swiss-Prot Accession number P40352	4.2
783	X58839	Acholeplasma virus MV-L1 DNA for complete circular genome	0.022	3273189	(AB008757) subunit II of c(o/b)3-type cytochrome c oxidase [Bacillus stearothermophilus]	4.1
784	M26185	Mouse c-myb oncogene, exon 1 and exon 2 (partial).	0.022	138592	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) >gi\|72270\|pir\|\|VJFF1 vitellogenin I precursor unnamed protein product [Drosophila melanogaster]	2.5
785	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene, complete cds	0.022	2088768	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	0.86
786	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.022	1352361	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi\|531456 (U12895) egr1 [Danio rerio] rerio]	0.36
787	Z71500	S.cerevisiae chromosome XIV reading frame ORF YNL224c	0.022	1708875	PUTATIVE TUMOR SUPPRESSOR LUCA15 sapiens]	0.16
788	D10471	Herpes simplex virus type 2 genomic DNA for 0.74-0.84 region, complete cds	0.022	3132276	(AB011486) short ORF [TT virus]	0.13
789	U43082	Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds	0.022	3319720	(AL031035) putative aldehyde dehydrogenase [Streptomyces coelicolor]	0.011

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens simple				
790	X86913	tandem repeat DNA (clone wg3a6)	0.021	<NONE>	<NONE>	<NONE>
791	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
792	U34016	Nannostomus sp. large subunit rRNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.	0.021	<NONE>	<NONE>	<NONE>
793	X00845	Yeast mitochondrial genes for 15S rRNA and tRNA-Trp	0.021	<NONE>	<NONE>	<NONE>
794	AB012113	Homo sapiens gene for CC chemokine PARC precursor, complete cds	0.021	<NONE>	<NONE>	<NONE>
795	U62395	Daucus carota globulin-like protein (Gea8) gene, complete cds	0.021	<NONE>	<NONE>	<NONE>
796	M22718	P.falciparum actin II gene, complete cds.	0.021	2623773	(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	8.8
797	U27118	Arabidopsis thaliana glutamyl-tRNA reductase	0.021	3549885	(AJ006631) cysteine-rich secretory protein-1 [Equus caballus]	8.8
798	X99832	H.sapiens CLN3 gene, complete CDS	0.021	262249	(S52010) orf1 5' of EpoR [mice, Peptide, 85 aa] [Mus sp.]	8.7
799	AF016266	Homo sapiens TRAIL receptor 2 mRNA, complete cds	0.021	729048	SUCCINYL-COA:COENZYME A TRANSFERASE transferase [Clostridium kluyveri]	8.7
800	Z92541	Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-13 contains lactase-phlorizin hydrolase (LCT)	0.021	585820	LIPOPOLYSACCHARIDE 1,2-N-ACETYLGLUCOSAMINETRANSFERASE >gi\|466761 (U00039) rfaK [Escherichia coli] >gi\|1790053 (AE000440) probably hexose transferase; lipopolysaccharide core biosynthesis	5.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		dopamine D2				
801	S58588	receptor [human, brain, Genomic, 3794 nt, segment 4 of 5]	0.021	2677620	(Y08029) NAD(P)(+)--arginine ADP-ribosyltransferase [Oryctolagus cuniculus]	5.1
802	M60522	Rat nerve growth factor-inducible protein (VGF) gene, complete cds.	0.021	4103934	(AF030050) replication factor C [Rattus norvegicus]	3.1
803	AF045654	Gallus gallus neuregulin beta-1a mRNA, complete cds	0.021	2746829	(AF040647) No definition line found [Caenorhabditis elegans]	3.0
804	M69023	Human globin gene.	0.021	3880259	(Z82056) T26H5.8 [Caenorhabditis elegans] >gi\|3880787\|gnl\|PID\|e1350288 (AL032620) T26H5.8	2.4
805	Z65960	H.sapiens CpG DNA, clone 69d2, reverse read cpg69d2.rt1b .	0.021	1707245	(U80845) similar to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	0.79
806	X97073	A.oligospora gene encoding lectin	0.021	116949	CORE ANTIGEN >gi\|73601\|pir\|\|NKVLC2 core antigen - woodchuck hepatitis virus 2 >gi\|336135	0.47
807	X56491	D. melanogaster mRNA for gene containing opa repetitive element	0.021	2842750	HOMEOBOX PROTEIN DLX-7 >gi\|1620520	0.16
808	L78760	Homo sapiens (subclone 1_f6 from P1 H31) DNA sequence	0.021	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.15
809	AB007864	Homo sapiens KIAA0404 mRNA, partial cds	0.021	118144	CYSTEINE SYNTHASE A (O-ACETYLSERINE SULFHYDRYLASE A) (O-ACETYLSERINE (THIOL)-LYASE A) (CSASE A) >gi\|68323\|pir\|\|SYEBAC cysteine synthase (EC 4.2.99.8) A - Salmonella typhimurium >gi\|153935 (M21450) cysK protein [Salmonella typhimurium]	0.12
810	AL021932	Mycobacterium tuberculosis H37Rv complete genome; segment 22/162	0.021	2909514	(AL021932) hypothetical protein Rv0439c	7e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
811	U89991	Hypocrea jecorina mannose-1-phosphate guanylyltransferase (MPG1) mRNA, complete cds	0.021	3581924	(AL031538) mannose-1-phosphate guanyltransferase [Schizosaccharomyces pombe]	6e-20
812	X00641	Sugar beet mitochondrial minicircle pO sequence	0.020	<NONE>	<NONE>	<NONE>
813	Z50097	D.melanogaster mRNA for hdc protein.	0.020	<NONE>	<NONE>	<NONE>
814	AF044866	Phoebis sennae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs	0.020	<NONE>	<NONE>	<NONE>
815	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
817	AE001405	Plasmodium falciparum chromosome 2, section 42 of 73 of the complete sequence	0.020	2196776	(AF003342) bunched gene product [Drosophila melanogaster]	8.4
818	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	627071	histidine-rich protein - Plasmodium lophurae	2.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
819	Y13304	Hylobates hoolock mitochondrial DNA for cytb gene, Horace	0.020	285580	(D10043) ORF [Acetobacter pasteurianus]	2.1
820	Z66539	H.sapiens creatine transporter gene	0.020	1703594	(U80439) coded for by C. elegans cDNA yk7c8.5; coded for by C. elegans cDNA yk133b3.5; coded for by C. elegans cDNA yk65a4.5; coded for by C. elegans cDNA yk7c8.3; coded for by C. elegans cDNA CEESQ66F; coded for by C. elegans cDNA yk65a4.3;...	0.98
821	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.020	1352361	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi\|531456 (U12895) egr1 [Danio rerio] rerio]	0.72
822	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	465569	HYPOTHETICAL 38.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION >gi\|405956 (U00009) ORF_ID:o349#4; similar to [SwissProt Accession Number P33015] [Escherichia coli] >gi\|1736693\|gnl\|PID\|d1016570 Number P33015] [Escherichia coli] >gi\|1788323 (AE000292) putative transport system permease protein [Escherichia coli]	0.43
823	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	1709751	COENZYME PQQ SYNTHESIS PROTEIN F synthesis F - Pseudomonas fluorescens >gi\|929802	0.42

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III >gi\|102507\|pir\|\|S15787 hypothetical protein 1 (cosmid ZK637) - Caenorhabditis elegans Genefinder; cDNA EST yk217b5.3 comes from this gene; cDNA EST yk217b5.5 comes from this gene; cDNA EST yk340g12.3 comes from this gene; cDNA EST yk340g12.5 comes from this gene; cDNA EST yk428c5.5 co...	
824	AJ005015	Homo sapiens mRNA for putative SMC-like protein, partial	0.020	267449		1e-12
825	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.020	1109847	(U41538) No definition line found [Caenorhabditis elegans]	1e-22
826	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	132836	60S RIBOSOMAL PROTEIN L28 protein L28 [Rattus norvegicus]	5.7
827	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.019	2633401	(Z99109) similar to DNA exonuclease	4.5
828	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	2492604	MULTIDRUG RESISTANCE PROTEIN CDR2 albicans]	4.4
829	U67538	Methanococcus jannaschii section 80 of 150 of the complete genome	0.019	1723566	PUTATIVE GLUCOSYLTRANSFERASE C17C9.07 >gi\|1314159\|gnl\|PID\|e241760 (Z73099) SPAC17C9.07, putative glucosyl transferase len: 501, similar to SW:ALG8_YEAST P40351 glucosyltransferase ALG8 pombe]	2.7
830	U56088	Human periodic tryptophan protein 2 (PWP2) gene, exons 3 to 14	0.019	2144804	collagen alpha 1(II) chain - bovine	0.040
831	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.018	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	7.2

-	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
832	AF026258	Onobrychis viciifolia chalcone synthase (CHS) mRNA, complete cds	0.018	763076	(Z48799) ZP3 [Cyprinus carpio] >gi\|777724 (L41637) egg membrane protein [Cyprinus carpio]	5.2
833	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.009	3955011	(AJ005438) beta adrenoreceptor B	0.60
834	X71603	C.jejuni VS1 DNA > :: emb\|A39603\|A39603 Sequence 2 from Patent WO9417205 > :: gb\|I76090\|I76090 Sequence 2 from patent US 5691138	0.008	<NONE>	<NONE>	<NONE>
835	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.008	138116	HEAD FIBER PROTEIN (LATE PROTEIN GP8.5) >gi\|75846\|pir\|\|WMBP8H gene 8.5 protein - phage PZA >gi\|216057 (M11813) head fiber protein	8.1
836	X91751	Bovine herpesvirus type 1 UL7 gene	0.008	1711436	SUPEROXIDE DISMUTASE (FE) 1.15.1.1) (Fe) - Pseudomonas aeruginosa >gi\|409767	5.9
837	M95594	Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene, complete cds.	0.008	683698	(Z48229) orf1 gene product [Saccharomyces cerevisiae]	1e-06
838	U67465	Methanococcus jannaschii section 7 of 150 of the complete genome	0.008	3874664	(Z68493) predicted using Genefinder	1e-07
839	X72388	B.taurus mRNA for filensin	0.008	100174	1-aminocyclopropane-1-carboxylate synthase	7e-09
840	U22398	Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.	0.008	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	2e-18
841	L42546	Xenopus laevis LIM class homeodomain protein	0.007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
842	AF041428	ribosomal protein s4 X isoform gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
843	AF000227	Secale cereale omega secalin gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D86254	Human MHC (HLA) DRB intron 1 DNA, partial sequence	0.007	<NONE>	<NONE>	<NONE>
845	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
846	Y07738	M.musculus gene for vimentin	0.007	<NONE>	<NONE>	<NONE>
847	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	<NONE>	<NONE>	<NONE>
848	AF055119	Homo sapiens alpha-tectorin (TECTA) gene, exon 6	0.007	<NONE>	<NONE>	<NONE>
849	M61195	Zucchini 1-aminocyclopropane-1-carboxylate synthase	0.007	<NONE>	<NONE>	<NONE>
850	Y11050	Homo sapiens DSG3 gene, partial intron and partial exon 6, 140 bp	0.007	<NONE>	<NONE>	<NONE>
851	X61204	M.voltae vhuD, vhuG, vhuA, vhuU & vhuB genes	0.007	<NONE>	<NONE>	<NONE>
852	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	S43882	telomere: {minichromosome, repeats} [Trypanosoma brucei, Genomic, 1170 nt]	0.007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
854	L32674	Geomydoecus nadleri mitochondrial cytochrome oxidase I gene, partial cds.	0.007	<NONE>	<NONE>	<NONE>
855	U58732	Caenorhabditis elegans cosmid F48D6.	0.007	<NONE>	<NONE>	<NONE>
856	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
857	Z35284	H.sapiens mRNA for MDR3 P-glycoprotein	0.007	1730696	HYPOTHETICAL 121.1 KD PROTEIN IN BIO3-HXT17 INTERGENIC REGION PRECURSOR YNR067c - yeast (Saccharomyces cerevisiae)	9.5
858	X15217	Human sno oncogene mRNA for snoA protein, ski-related	0.007	902455	(U24203) membrane protein [Escherichia coli]	8.8
859	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	1684636	(Y09454) ORF3 [Lactobacillus casei bacteriophage A2]	8.3
860	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	3878803	(Z48795) R05H5.7 [Caenorhabditis elegans]	8.3
861	S76317	119=180-200 kda membrane protein scavenger receptor homolog {clone 18, intron and flanking exons 14 and 15} [sheep, lymph node, lymphocytes, Genomic, 308 nt, segment 2 of 2]	0.007	294747	(L08174) ORF2 [Romanomermis culicivorax]	7.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
862	D88084	Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)5'exon	0.007	2555187	(AF026789) vitellogenin [Pimpla nipponica]	6.9
863	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	115978	CD30L RECEPTOR PRECURSOR (LYMPHOCYTE ACTIVATION ANTIGEN	6.5
864	D87120	Homo sapiens mRNA for GS3786, complete cds	0.007	3879589	(Z50875) Prolific rich domain, cDNA EST EMBL:D35637 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes fr... >gi\|3880965\|gnl\|PID\|e1350578 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes ...	5.1
865	X68793	H.sapiens gene for antithrombin III	0.007	2358285	(AF010403) ALR [Homo sapiens]	3.8
866	AJ001596	Danio rerio mRNA for opioid receptor homologue	0.007	2507509	HYPOTHETICAL 29.8 KD PROTEIN IN HOLB-PTSG INTERGENIC REGION >gi\|1787342 (AE000210) orf, hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli]	1.9
867	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene, complete cds	0.007	2088768	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	1.9
868	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	1710105	UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE UDP-N-acetylglucosamine 2-epimerase [Plasmid pWQ799]	1.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Zebrafish retinoic				
869	L03398	acid receptor alpha 2.A	0.007	2239219	(Z97210) hypothetical protein	0.77
870	D63484	Human mRNA for KIAA0150 gene, partial cds	0.007	19917	(Z14014) Pistil extensin like protein, partial CDS only	0.61
871	M31483	Maize glyceraldehyde 3-phosphate dehydrogenase, 3' end.	0.007	543068	mucin, tracheobronchial - dog >gi\|402558	0.45
872	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.007	2494941	ALPHA-2B ADRENERGIC RECEPTOR adrenoceptor [Cavia porcellus] >gi\|1587159\|prf\|\|2206293B adrenoceptor alpha2B [Cavia porcellus]	0.42
873	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.007	1110587	(S79410) nuclear localization signals Peptide, 140 aa] [Mus sp.]	0.26
874	X88931	H.sapiens PAL2A gene	0.007	1706176	CUTINASE TRANSCRIPTION FACTOR 1 ALPHA >gi\|1262912 (U51671) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]	0.21
875	S74155	zRAR alpha =retinoic acid receptor alpha [zebrafish, embryos, mRNA, 1773 nt]	0.007	2239219	(Z97210) hypothetical protein	0.11
876	M74193	Petromyzon marinus plasma albumin mRNA, complete cds.	0.007	730888	OCTAPEPTIDE-REPEAT PROTEIN T2	0.011
877	U03673	Saccharomyces cerevisiae Spp41p (SPP41) gene, complete cds.	0.007	3820885	(AL033126) 65G3.k [Drosophila melanogaster]	0.001
878	D37766	Homo sapiens mRNA for Laminin-5 beta3 chain, complete cds	0.007	1235974	(X96713) collagen [Globodera pallida]	3e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
879	AF022388	elegans putative transcription factor MAB-3 (mab-3) gene, complete cds	0.007	3747107	(AF095741) unknown [Rattus norvegicus]	5e-09
880	U89984	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds	0.007	1890281	(U89984) transformation-sensitive protein homolog	2e-09
881	AB020689	Homo sapiens mRNA for KIAA0882 protein, partial cds	0.007	3880809	(AL021485) similar to Probable rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ... Probable rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ...	1e-23
882	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
883	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
884	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
885	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
886	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>
887	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
888	M80529	Rattus norvegicus ceruloplasmin gene, exon 1 and 5' flank	0.006	<NONE>	<NONE>	<NONE>
889	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	99408	hypothetical protein 6 - Chlamydomonas reinhardtii transposon >gi\|1360717\|gnl\|PID\|e33461 reinhardtii]	9.6
890	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.006	4039024	(AF039110) polyprotein [Rubella virus]	9.3
891	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	160533	(M94428) merozoite surface antigen 1 [Plasmodium vivax]	7.5
892	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	4019458	(AF093984) envelope glycoprotein [Human immunodeficiency virus type 1]	7.0
893	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	6.8
894	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	102059	promastigote surface antigen-2 (clone 4.6) - Leishmania major (fragment) >gi\|9583 (X57135) surface antigen P2 [Leishmania major]	2.4
895	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	3171241	(AF067204) transcription factor BF-1 [Danio rerio]	1.0
896	X99384	M.musculus mRNA for paladin gene	0.003	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
897	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.003	<NONE>	<NONE>	<NONE>
898	AE001148	Borrelia burgdorferi (section 34 of 70) of the complete genome	0.003	4160388	(AJ011856) ORF Q0255 [Saccharomyces cerevisiae]	7.6
899	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.003	1709213	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)	1.5
900	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
901	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
902	AF104631	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
903	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
904	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
905	M21339	Human non-histone chromosomal protein HMG-14 gene, complete cds.	0.002	<NONE>	<NONE>	<NONE>
906	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human h-lys gene for				
907	X57103	lysozyme (upstream region)	0.002	<NONE>	<NONE>	<NONE>
908	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
909	U01066	Human CD4 promoter, partial sequence.	0.002	<NONE>	<NONE>	<NONE>
910	L28094	Barley mRNA sequence.	0.002	<NONE>	<NONE>	<NONE>
911	AD000833	Homo sapiens DNA from chromosome 19-cosmid f19399 (~17 kb EcoRI restriction fragment)	0.002	<NONE>	<NONE>	<NONE>
912	AJ011701	Homo sapiens TRHR gene promoter and exons 1-2, partial	0.002	<NONE>	<NONE>	<NONE>
913	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
914	AF037062	Homo sapiens retinol dehydrogenase gene, complete cds	0.002	<NONE>	<NONE>	<NONE>
915	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
916	U67608	Methanococcus jannaschii section 150 of 150 of the complete genome	0.002	<NONE>	<NONE>	<NONE>
917	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
918	Z46736	H.sapiens DNA for repeat region (ABM-C82)	0.002	<NONE>	<NONE>	<NONE>
919	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		X.laevis mRNA for				
920	Z85983	NOVA protein	0.002	<NONE>	<NONE>	<NONE>
921	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
922	S61977	medium-chain acyl-CoA dehydrogenase {exon 10, intron 10} [human, Genomic, 1407 nt]	0.002	<NONE>	<NONE>	<NONE>
923	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	<NONE>	<NONE>	<NONE>
924	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	<NONE>	<NONE>	<NONE>
925	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
926	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
927	X51646	H.sapiens DNA for dopamine D2 receptor gene	0.002	3329125	(AE001337) Yop C/Gen Secretion Protein D [Chlamydia trachomatis]	9.5
928	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	465762	HYPOTHETICAL 112.1 KD PROTEIN C06G4.1 IN CHROMOSOME III >gi\|630524\|pir\|\|S44748 C06G4.1 protein - Caenorhabditis elegans >gi\|409292 (L25598) homology with vigilin; coded for by C. elegans cDNA GenBank:M88954 (CEL12C9); putative [Caenorhabditis	8.9
929	U48478	Human skeletal muscle ryanodine receptor gene	0.002	2137221	co-repressor protein - mouse >gi\|642619	6.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
930	AF100694	Pontin52 mRNA, complete cds	0.002	806536	(Z22520) membrane protein [Bacillus acidopullulyticus]	6.3
931	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	3881055	(AL023844) Y48A6B.1 [Caenorhabditis elegans]	5.8
932	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.002	3878330	(Z81097) K07A1.4 [Caenorhabditis elegans]	4.8
933	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	137640	REPLICATION PROTEIN E1 papillomavirus	4.0
934	AF019660	Mus musculus nuclear orphan receptor RORgamma	0.002	1330365	(U58757) similar to nucleotide pyrophosphatases	3.9
935	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	1785972	(U46951) ORF5; Method: conceptual translation supplied by author	3.7
936	V00508	Human gene for epsilon-globin.	0.002	1333804	(X56082) protease [Ruminococcus flavefaciens]	3.5
937	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	4153876	(AC005531) similar to mouse homeodomain-interacting protein kinase 2; similar to AF077659 (PID:g3702958)	3.0
938	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	1070461	ornithine carbamoyltransferase (EC 2.1.3.3) - yeast (Saccharomyces cerevisiae) >gi\|929866 (X83502) pid:e130025 [Saccharomyces cerevisiae] >gi\|1008256	2.8
939	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	3450883	(AF083334) fibroin [Antheraea pernyi]	1.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
940	X06286	Drosophila melanogaster Gart locus with genes for GARS=phosphoribosylamineglycine ligase, AIRS=phosphoribosylformylglycinamidine cyclo-ligase, GART=glycinamide ribotide transformylase > :: gb\|J02527\|DROGART D.melanogaster Gart gene encoding two polypeptides with GAR synthase, AIR synthase, and GAR transformylase enzyme activities and a pupal cuticle gene nested within intron A of the Gart gene.	0.002	2662054	(AB004651) isocitrate lyase	1.5
941	AF015812	Homo sapiens RNA helicase p68 (HUMP68) gene, complete cds	0.002	3641659	(AB008374) alpha 3 type I collagen	1.1
942	X78925	H.sapiens HZF2 mRNA for zinc finger protein	0.002	141624	ZINC FINGER PROTEIN ZFP-37 (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN)	1.0
943	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	3879997	(Z49071) weak similarity with mu-type opioid receptor (Swiss Prot accession number (P33535)	1.0
944	Z69639	Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.	0.002	3523162	(AF076292) TGF-beta/activin signal transducer FAST-1p	0.81

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
945	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	2984161	(AE000761) hypothetical protein [Aquifex aeolicus]	0.80
946	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	101830	hypothetical protein B - chestnut blight fungus	0.72
947	AF017307	Homo sapiens Ets-related transcription factor (ERT) mRNA, complete cds	0.002	200531	(M18071) prion protein [Mus musculus]	0.72
948	U11383	Drosophila melanogaster Ovo-1028aa (ovo) mRNA, complete cds.	0.002	2465207	(AF016045) OVO-like 1 binding protein [Homo sapiens]	0.35
949	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	3834294	(U80846) No definition line found [Caenorhabditis elegans]	0.29
950	AF086315	Homo sapiens full length insert cDNA clone ZD52F10	0.002	545067	(S68356) action potential broadening potassium channel=Shab [Aplysia, bag cell neurons, head ganglia, Peptide, 905 aa] [Aplysia] >gi\|743110\|prf\|\|2011375A K channel [Aplysia californica]	0.15
951	X53096	S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease	0.002	2529575	(AF018164) kinesin-like protein 3C [Homo sapiens]	0.11
952	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	729918	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)	0.092
953	X73973	G.gallus RAR-gamma2 mRNA for retinoic acid receptor	0.002	586122	TRICHOHYALIN >gi\|423321\|pir\|\|A40691 trichohyalin - sheep >gi\|295941 (Z18361) trichohyalin	0.073
954	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	1017427	(X90569) elastic titin [Homo sapiens]	0.013

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		D.melanogaster			(U88169) similar to	
955	M35887	defective chorion-1 fc125 (dec-1) gene, complete cds.	0.002	1825606	molybdoterin biosynthesis MOEB proteins [Caenorhabditis elegans]	0.008
956	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.002	1825593	(U88167) D2092.2 gene product [Caenorhabditis elegans]	1e-06
957	AF033929	Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence	9e-04	<NONE>	<NONE>	<NONE>
958	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-04	<NONE>	<NONE>	<NONE>
959	AF029062	Homo sapiens DEAD-box protein (BAT1) gene, partial cds	8e-04	<NONE>	<NONE>	<NONE>
960	U70671	Human ataxin-2 related protein mRNA, partial cds	8e-04	<NONE>	<NONE>	<NONE>
961	AF051709	Dendrocopos leucopterus clone 2 microsatellite HrU2 repeat region	8e-04	<NONE>	<NONE>	<NONE>
962	X14077	Pea phy gene for phytochrome apoprotein	8e-04	<NONE>	<NONE>	<NONE>
963	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	8e-04	457146	(L27838) rhoptry protein [Plasmodium yoelii]	9.6
964	AF077344	Homo sapiens cartilage-derived C-type lectin	8e-04	3702123	(AJ011707) TraD protein [Escherichia coli]	8.5
965	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	8e-04	2570059	(AJ004687) N-4 cytosine-specificmMethyltransferase [Neisseria gonorrhoeae]	6.8
966	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1345859	COPPER TRANSPORT PROTEIN CTR1 transport protein - yeast (Saccharomyces cerevisiae) gene product [Saccharomyces cerevisiae]	6.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
967	AF031403	MLL/AF4 translocation breakpoint t(4;11)(q21;23)	8e-04	2498926	SMALL PROTEIN B HOMOLOG A43259, from E. hirae [Mycoplasma pneumoniae]	6.6
968	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7.	8e-04	1488070	(U63997) putative transposase [Enterococcus faecium]	5.2
969	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	8e-04	1493833	(U47323) stromal cell protein [Mus musculus]	3.2
970	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds	8e-04	1346101	4-AMINOBUTYRATE AMINOTRANSFERASE TRANSAMINASE) (GABA AMINOTRANSFERASE) homolog - smut fungus (Ustilago maydis) >gi\|881562 Emericella nidulans gamma-amino-n-butyrate transaminase Swiss-Prot Accession Number P14010 [Ustilago maydis]	0.83
971	U37452	Human Down Syndrome region of chromosome 21 genomic sequence, clone A31D6-1C5.	8e-04	4164069	(AF111093) latrophilin 3 splice variant bbah [Bos taurus]	0.26
972	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1352877	HYPOTHETICAL 13.0 KD PROTEIN IN RAD26-GEF1 INTERGENIC REGION >gi\|1077881\|pir\|\|S57057 probable membrane protein YJR038c - yeast (Saccharomyces cerevisiae) >gi\|1015688 (Z49538) ORF YJR038c putative [Saccharomyces cerevisiae]	0.23
973	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-04	1788557	(AE000312) orf, hypothetical protein [Escherichia coli]	0.19

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
974	X83872	H.vulgaris mRNA for cAMP response element binding protein	8e-04	1175386	HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I >gi\|2130289\|pir\|\|S58305 hypothetical protein SPAC18B11.06 - fission yeast hypothetical protein [Schizosaccharomyces pombe]	0.005
975	M32514	Rat simple sequence DNA, clone 5.	8e-04	2394492	(AF024502) No definition line found [Caenorhabditis elegans]	0.002
976	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
977	X89211	H.sapiens DNA for endogenous retroviral like element	8e-04	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	3e-04
978	U14391	Human myosin-IC mRNA, complete cds.	8e-04	3142302	(AC002411) Strong similarity to myosin heavy chain gb\|Z34293 from A. thaliana. [Arabidopsis thaliana]	4e-16
979	L13612	Drosophila melanogaster dead-box protein D.melanogaster DEAD-box gene, complete CDS	8e-04	3776027	(AJ010475) RNA helicase [Arabidopsis thaliana]	9e-24
980	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
981	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
982	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
983	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22 Contains ESTs, complete sequence [Homo sapiens]	7e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
984	AB012106	Brassica rapa mRNA for SRK45, complete cds	7e-04	<NONE>	<NONE>	<NONE>
985	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
986	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
987	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
988	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	<NONE>	<NONE>	<NONE>
989	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
990	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
991	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
992	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
993	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
994	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
995	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.3
996	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	3876455	(Z93380) predicted using Genefinder; similar to 7tm receptor protein [Caenorhabditis elegans]	7.1
997	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	2128771	hypothetical protein MJ1293 - Methanococcus jannaschii >gi\|1591931 (U67570) M. jannaschii predicted coding region MJ1293 [Methanococcus jannaschii]	6.2
998	U09412	Human zinc finger protein ZNF134 mRNA, complete cds	7e-04	1083336	glutathione transferase (EC 2.5.1.18) piA - mouse	5.4
999	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	473515	(M17619) NADH dehydrogenase subunit ND4 [Asterina pectinifera]	3.7
1000	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	1724097	(U79772) female sex protein [Mercurialis annua]	3.3
1001	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	1197103	(D49747) core, env, and part of E2/NS1	3.2
1002	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	7e-04	345372	unc-5 protein, long form - Caenorhabditis elegans >gi\|258529\|bbs\|118648 (S47168) UNC-5=immunoglobulin and thrombospondin type 1 transmembrane protein {alternatively spliced} aa] [Caenorhabditis elegans] >gi\|2662596 (AF036698) C. elegans UNC-5 (NID:g25852)	2.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1003	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	4204220	(AB022866) mobilization protein	2.5
1004	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	3201550	(Y17116) fibrinogen-binding protein	2.4
1005	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	1174264	(U45966) polyprotein [Hepatitis G virus]	0.73
1006	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	135308	TRANSCRIPTION FACTOR JUN-D	0.065
1007	X98745	H.sapiens EWS gene, intron 6, polymorphism	7e-04	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.001
1008	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	1633564	(U47924) C8 [Homo sapiens]	9e-09
1009	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	6e-04	284171	Ig epsilon chain C region form 3 - human	1.3
1010	AB012106	Brassica rapa mRNA for SRK45, complete cds	6e-04	3845262	(AE001414) BRAHMA ortholog (DNA helicase superfamily II)	0.25
1011	AL034404	Human DNA sequence from clone 417C12 on chromosome Xp22.11 22.2, complete sequence [Homo sapiens]	3e-04	<NONE>	<NONE>	<NONE>
1012	M99701	Homo sapiens (pp21) mRNA, complete cds.	3e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1013	U00227	Ovis aries Merino breed DR beta-chain antigen binding domain, MHC class II DRB (Ovar-DRB24) gene, partial cds.	3e-04	<NONE>	<NONE>	<NONE>
1014	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1015	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-04	999418	(L19655) ORF [Tomato ringspot virus]	8.3
1016	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-04	2367460	(AF011415) putative pheromone receptor [Mus musculus]	7.0
1017	AJ010737	Mus musculus DNA for microsatellite 3kb upstream lbp gene	3e-04	4106549	(AF104411) neuronal-specific septin 3 [Mus musculus]	5.5
1018	AF053137	Homo sapiens histone deacetylase 3 gene, exons 4, 5, 6, 7, 8, 9, and 10	3e-04	416702	NADH-DEPENDENT FLAVIN OXIDOREDUCTASE acid-inducible - Eubacterium sp >gi\|1381570 (U57489) NADH:flavin oxidoreductase [Eubacterium sp. VPI 12708]	5.3
1019	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	3e-04	1785789	(Y08502) orf111d [Arabidopsis thaliana]	5.1
1020	AC004173	Homo sapiens clone UWGC:y23x011 from 6p21, complete sequence [Homo sapiens]	3e-04	558521	(D28917) polyprotein [Hepatitis C virus]	1.1
1021	X57025	Human IGF-I mRNA for insulin-like growth factor I	3e-04	4206707	(AF118122) putative outer membrane protein OmpU	0.65
1022	X77090	H.sapiens IL-1Ra gene.	3e-04	1065941	(U40799) F42C5.7 gene product [Caenorhabditis elegans]	0.12

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Pseudorabies virus				
1023	M34651	with upstream and downsteam sequences.	3e-04	2746853	(AF040650) contains similarity to sodium-potassium-chloride cotransport proteins	7e-05
1024	Z36011	S.cerevisiae chromosome II reading frame ORF YBR142w	3e-04	2500537	PROBABLE ATP-DEPENDENT RNA HELICASE HAS1 >gi\|626265\|pir\|\|S47451 hypothetical protein YMR290c RNA helicase [Saccharomyces cerevisiae]	4e-08
1025	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	6e-14
1026	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	3e-04	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	9e-15
1027	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	1e-17
1028	X79811	S.cerevisiae ACT3 gene	3e-04	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-31
1029	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1030	M22970	Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1 to 3.	2e-04	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA sequence from cosmid N2E9 on chromosome 22. Contains EST, complete sequence [Homo sapiens]				
1031	Z68686		2e-04	<NONE>	<NONE>	<NONE>
1032	X95154	H.sapiens brca2 gene exon 4 > :: emb\|A62779\|A62779 Sequence 20 from Patent WO9719110	2e-04	<NONE>	<NONE>	<NONE>
1033	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1034	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1035	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	2e-04	<NONE>	<NONE>	<NONE>
1036	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1037	AC000958	Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence	2e-04	<NONE>	<NONE>	<NONE>
1038	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	2e-04	2501523	CD59 GLYCOPROTEIN PRECURSOR	7.1
1039	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	2765360	(Y13925) cathepsin L2 [Penaeus vannamei]	6.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RNA POLYMERASE	
1040	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	2e-04	133636	>gi\|67126\|pir\|\|RRXPLC RNA-directed RNA polymerase (EC 2.7.7.48) - lymphocytic choriomeningitis virus (strain Armstrong 53b) >gi\|331369	5.2
1041	AB012106	Brassica rapa mRNA for SRK45, complete cds	2e-04	3822155	(AF074613) type II secretion protein [Escherichia coli O157:H7]	4.0
1042	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	1718125	REGULATORY PROTEIN E2 >gi\|1020222 type 36]	0.38
1043	X17058	Sus scrofa mRNA for glucose transporte protein	2e-04	3341906	(AB009593) xylose transporter	2e-15
1044	AF008216	Homo sapiens candidate tumor suppressor pp32r1	1e-04	<NONE>	<NONE>	<NONE>
1045	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	1e-04	624126	(U42580) a65L [Paramecium bursaria Chlorella virus 1]	7.9
1046	L14930	Glycine max (Rab7p) mRNA, complete cds.	9e-05	<NONE>	<NONE>	<NONE>
1047	AJ009970	Mus musculus thromboxane A2 receptor gene, exon 3, partial	9e-05	<NONE>	<NONE>	<NONE>
1048	Y11896	M.musculus mRNA for Brx gene, partial	9e-05	<NONE>	<NONE>	<NONE>
1049	L10832	Polistes annularis (clone pan48AAT) tandem repeat region.	9e-05	<NONE>	<NONE>	<NONE>
1050	AF055011	Homo sapiens clone 24587 mRNA sequence	9e-05	3880586	(Z79758) cDNA EST EMBL:D28009 comes from this gene; cDNA EST EMBL:D28008 comes from this gene; cDNA EST EMBL:D32478 comes from this gene; cDNA EST EMBL:D34508 comes from this gene; cDNA EST EMBL:D37581 comes from this gene; ...	7.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1051	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-05	3024292	RHODOPSIN >gi\|2290717 (AF000947) rhodopsin [Sepia officinalis]	6.7
1052	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a .	9e-05	3885496	(AF064825) heparin/heparan sulfate N-acetylglucosaminyl N-deacetylase/N-sulfotransferase [Bos taurus]	0.65
1053	D87451	Human mRNA for KIAA0262 gene, complete cds	9e-05	3874739	(Z66495) similar to claustrin like	0.004
1054	L37092	Mus musculus cyclin-dependent kinase homologue	9e-05	3080513	(AL022598) hypothetical protein	4e-09
1055	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1056	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1057	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1058	D10102	Homo sapiens DNA from cosmid clone:844, GT repeat sequence	8e-05	<NONE>	<NONE>	<NONE>
1059	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	8e-05	1176475	HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION >gi\|1078237\|pir\|\|S56849 probable membrane protein YJL073w - yeast (Saccharomyces cerevisiae) >gi\|895898 (X88851) hypothetical protein YJL073w [Saccharomyces cerevisiae]	6.0
1060	X71934	H.sapiens XB gene for tenascin-X, repeat XIII	8e-05	285207	microtubule-associated protein, 110K tau - rat >gi\|207158 (M84156) big tau [Rattus norvegicus]	3.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1061	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	4049682	(AF063866) ORF MSV092 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	2.1
1062	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	8e-05	3861019	(AJ235271) unknown [Rickettsia prowazekii]	5e-14
1063	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1064	L04193	Human lens membrane protein (mp19) gene, exon 11.	7e-05	<NONE>	<NONE>	<NONE>
1065	X61609	B.napus gene for LHC II Type III chlorophyll a/b binding protein	7e-05	2132314	hypothetical protein YPR174c - yeast similarity to a nuclear lamin from C. elegans (PIR accession number S42257) [Saccharomyces cerevisiae]	8.9
1066	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-05	2979422	(AB006757) PCDH7 (BH-Pcdh)c [Homo sapiens]	5.7
1067	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-05	2493696	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi\|1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]	5.2
1068	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-05	2501029	PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (LEUCINE--TRNA LIGASE) (LEURS) KIAA0028 [Homo sapiens]	1.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1069	Z68758	sequence from cosmid cN85E10 on chromosome 22q11.2-qter	3e-05	<NONE>	<NONE>	<NONE>
1070	X60653	human Histone H3.3 pseudogene (CIR-456)	3e-05	<NONE>	<NONE>	<NONE>
1071	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a .	3e-05	1706241	GUANYLYL CYCLASE GC-E PRECURSOR cyclase receptor [Mus musculus]	9.6
1072	AF043251	Homo sapiens mitochondrial outer membrane protein (Tom40) gene, nuclear gene encoding mitochondrial protein, exons 1 through 6	3e-05	113980	AMINE OXIDASE [FLAVIN-CONTAINING] B oxidase (flavin-containing) (EC 1.4.3.4) B - human B [human, platelet, Peptide Partial, 520 aa] [Homo sapiens]	8.9
1073	M31104	Chicken progesterone receptor gene, encoding forms A and B, exons 1 and 2.	3e-05	1170841	IG GAMMA LAMBDA CHAIN V-II REGION	4.8
1074	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	543684	ribosomal protein S3 - Chlamydomonas humicola chloroplast (fragment)	4.2
1075	L22206	Human vasopressin receptor V2 gene, complete cds.	3e-05	791207	(U20615) Gnot1 homeodomain protein [Gallus gallus]	1.8
1076	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	3e-05	3237340	(AF033361) polyprotein [Hepatitis C virus]	0.94
1077	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2879805	(AL021813) hypothetical protein	0.001
1078	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	3877951	(Z81555) predicted using Genefinder	3e-07

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1079	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-05	<NONE>	<NONE>	<NONE>
1080	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	3880197	(Z81132) predicted using Genefinder	2.4
1081	AF087989	Homo sapiens full length insert cDNA clone YX29D10	2e-05	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	1.8
1082	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	474896	(L31967) mating type protein [Coprinus cinereus]	1.4
1083	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	2266988	(Y13274) M33 polycomb-like protein [Mus musculus]	0.62
1084	U67415	Equus caballus UCD-E-CA-467 dinucleotide repeat region, complete sequence	1e-05	<NONE>	<NONE>	<NONE>
1085	X67277	H.sapiens BGP gene for biliary glycoprotein, promoter region and exon 1	1e-05	<NONE>	<NONE>	<NONE>
1086	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	1e-05	<NONE>	<NONE>	<NONE>
1087	U88328	Mus musculus suppressor of cytokine signalling-3	1e-05	443877	(Z29457) core region; pid:g443877 [Hepatitis C virus] virus]	3.9
1088	Y12853	Homo sapiens P2X7 gene, exon 4-8	1e-05	3878726	(Z66498) similar to cuticle collagen; cDNA EST EMBL:D75584 comes from this gene	0.36
1089	AE001140	Borrelia burgdorferi (section 26 of 70) of the complete genome	1e-05	3860719	(AJ235270) GLUTAMYL-tRNA AMIDOTRANSFERASE SUBUNIT A (gatA) [Rickettsia prowazekii]	4e-15

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1090	AJ224112	Homo sapiens gamma-adaptin gene, exon 2 and flanking intronic sequences	9e-06	<NONE>	<NONE>	<NONE>
1091	AB000565	Homo sapiens DNA for repeat sequence Alu	9e-06	72879	translation initiation factor IF-2 - Escherichia coli	5.1
1092	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	9e-06	159975	(M65164) 51C surface protein [Paramecium tetraurelia]	4.8
1093	Z21677	Thermotoga maritima DNA for spc operon	9e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gi\|437926 (Z21677) ribosomal protein L2	7e-14
1094	AF031494	Drosophila hydei Dhc7 (Threads) mRNA, complete cds	9e-06	729377	DYNEIN BETA CHAIN, CILIARY sea urchin (Anthocidaris crassispina) chain [Anthocidaris crassispina]	4e-18
1095	AF051315	Homo sapiens placental protein 17a1 (PP17) mRNA, complete cds	4e-06	<NONE>	<NONE>	<NONE>
1096	AC001460	Homo sapiens (subclone 2_f4 from BAC H107) DNA sequence	4e-06	2648304	(AE000952) ISA1214-6, putative transposase	6.2
1097	X85030	H.sapiens mRNA for skeletal muscle-specific calpain	4e-06	4239857	(AB016726) calpain [Schistosoma japonicum]	0.006
1098	M75162	Human polymorphic arylamine N-acetyltransferase	3e-06	<NONE>	<NONE>	<NONE>
1099	AB009999	Rattus norvegicus mRNA for CDP-diacylglycerol synthase, complete cds	3e-06	3879045	(Z70309) R102.6 [Caenorhabditis elegans]	7.3
1100	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	3e-06	266529	MERCURIC REDUCTASE (HG(II) REDUCTASE) >gi\|418744\|pir\|\|S30168 mercury(II) reductase	6.5
1101	AB012190	Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds	3e-06	3877938	(Z79697) F58H10.1 [Caenorhabditis elegans]	6.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1102	AF041056	WSCR4 gene, exons 3 and 4	3e-06	1568583	(Z80775) hypothetical protein Rv0044c	1.9
1103	X00777	Mouse E(d) beta gene 5' flanking region and exon 1	3e-06	1680722	(U72497) fatty acid amide hydrolase [Rattus norvegicus]	0.008
1104	D21205	Human mRNA for estrogen responsive finger protein, complete cds	3e-06	563127	(U09825) acid finger protein [Homo sapiens]	1e-05
1105	Z47046	Human cosmid QLL2C9 from Xq28	1e-06	<NONE>	<NONE>	<NONE>
1106	L26261	Human MHC class III HLA-RP1 gene.	1e-06	<NONE>	<NONE>	<NONE>
1107	M13402	Rat 5S RNA gene, clone 5S-2.	1e-06	<NONE>	<NONE>	<NONE>
1108	X68793	H.sapiens gene for antithrombin III	1e-06	<NONE>	<NONE>	<NONE>
1109	AF003540	Homo sapiens Krueppel family zinc finger protein	1e-06	2507553	ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) Kruppel-related. [Homo sapiens]	0.098
1110	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1e-06	1330401	(U58762) T27F7.1 gene product [Caenorhabditis elegans]	0.015
1111	Z69925	Human DNA sequence from cosmid cN116A5, between markers D22S280 and D22S86 on chromosome 22q12 contains EST	9e-07	<NONE>	<NONE>	<NONE>
1112	D90217	S. cerevisiae gene for YmL33, mitochondrial ribosomal proteins of large subunit	9e-07	3879097	(Z81109) predicted using Genefinder; similar to sodium/phosphate transporter; cDNA EST yk326f6.3 comes from this gene; cDNA EST yk326f6.5 comes from this gene [Caenorhabditis elegans]	7.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U58755) coded for by C.	
1113	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-07	1330345	elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	2e-29
1114	AF086562	Homo sapiens full length insert cDNA clone ZE16C03	4e-07	1072210	(U40945) coded for by C. elegans cDNA yk74b9.3; coded for by C. elegans cDNA yk74b9.5; similar to repeat of calcium channel alpha subunits; similar to tetracycline resistance protein; similar to hypothetical protein in HSP30-PMP1 region (SP...	3.9
1115	L39062	Homo sapiens interleukin 9 receptor IL9R pseudogene, exons 1-9	4e-07	3879983	(Z46795) similar to transforming protein etc2; cDNA EST EMBL:D34137 comes from this gene; cDNA EST EMBL:D37172 comes from this gene; cDNA EST EMBL:D76266 comes from this gene; cDNA EST EMBL:D70493 comes from this gene; cDNA ...	3.3
1116	Z69364	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA. > :: emb\|Z69365\|HSL96F8A Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA.	4e-07	3493176	(AF022889) latent TGF beta binding protein [Mus musculus]	3.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for				
1117	D79986	KIAA0164 gene, complete cds	4e-07	4038031	(AC005936) hypothetical protein [Arabidopsis thaliana]	0.30
1118	D43950	Human mRNA for KIAA0098 gene, partial cds	3e-07	<NONE>	<NONE>	<NONE>
1119	AF037168	Arabidopsis thaliana DnaJ homologue (AtJ6) mRNA, complete cds	3e-07	3881075	(AL032657) predicted using Genefinder; similar to DnaJ domain ; Thioredoxin; cDNA EST yk433f3.5 comes from this gene; cDNA EST EMBL:D32359 comes from this gene; cDNA EST EMBL:D34721 comes from this gene; cDNA EST yk433f3.3 c...	3e-09
1120	X69838	H.sapiens mRNA for G9a	3e-07	3873414	(U00043) similar to D. melanogaster trithorax protein	3e-29
1121	AB011124	Homo sapiens mRNA for KIAA0552 protein, complete cds	2e-07	2618749	(U90880) hypothetical protein 2; predicted using XGrail	2.0
1122	K03012	Human cellular fms proto-oncogene, partial cds.	1e-07	<NONE>	<NONE>	<NONE>
1123	AB016195	Homo sapiens DNA, microsatellite and Alu repeat region	1e-07	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.095
1124	Y16795	Homo sapiens psihHaA pseudogene	4e-08	<NONE>	<NONE>	<NONE>
1125	AB012624	Homo sapiens FLI1 gene for ERGB transcription fuctor, intron 4 and partial cds	4e-08	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	3.6
1126	AJ131341	Homo sapiens ogg1 gene, exons 1-7	4e-08	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	3e-05
1127	L81902	Homo sapiens (subclone 1_c10 from P1 H69) DNA sequence	3e-08	4225950	(AJ132701) centaurin gamma1B	1.8
1128	Y17968	Gallus gallus mRNA for high mobility group 1 protein	3e-08	3041855	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	3e-31
1129	Y13901	Homo sapiens FGFR-4 gene	1e-08	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1130	L22024	Mesocricetus auratus serum amyloid P component gene, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1131	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1132	X14034	Human mRNA for phospholipase C > :: gb\|M37238\|HUMPL C Human phospholipase C mRNA, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1133	Z59381	H.sapiens CpG DNA, clone 152b10, forward read cpg152b10.ft1a .	1e-08	<NONE>	<NONE>	<NONE>
1134	L81839	Homo sapiens (subclone 2_h3 from P1 H43) DNA sequence	1e-08	<NONE>	<NONE>	<NONE>
1135	X14448	Human GLA gene for alpha-D-galactosidase A (EC 3.2.1.22)	1e-08	3334427	HYPOTHETICAL PROTEIN MJ1207 Methanococcus jannaschii >gi\|1591837 (U67562) protease synthase and sporulation negative regulator Pai1, putative [Methanococcus jannaschii]	9.1
1136	AL023774	Human DNA sequence from clone 799F15 on chromosome Xq25, complete sequence [Homo sapiens]	1e-08	1354935	(U58330) probable copper-transporting atpase	1.2
1137	X64639	H.sapiens DNA repetitive subtelomeric-like sequence (522 bp)	1e-08	77356	hypothetical 70K protein - eggplant mosaic virus	0.098
1138	U97058	Human HuD gene, 5'UTR	5e-09	3387886	(AF070530) unknown [Homo sapiens]	9.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1139	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-09	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	8.4
1140	AJ006587	Mus musculus mRNA for translation initiation factor eIF2 gamma X	5e-09	1872200	(U22376) alternatively spliced product using exon 13A	0.64
1141	Y11108	H.sapiens WNT8B gene	4e-09	2854198	(AF045646) contains similarity to collagens	4.0
1142	AE001223	Treponema pallidum section 39 of 87 of the complete genome	4e-09	3334189	CELL DIVISION PROTEIN FTSY HOMOLOG	1.5
1143	Z47046	Human cosmid QLL2C9 from Xq28	4e-09	104045	fibroblast growth factor receptor A1 precursor - African clawed frog >gi\|214894 (M55163) fibroblast growth factor receptor [Xenopus laevis]	1.3
1144	AG000746	Homo sapiens genomic DNA, 21q region, clone: T171Bm40	4e-09	113666	!!!! ALU CLASS A WARNING ENTRY !!!!	0.33
1145	M74002	Human arginine-rich nuclear protein mRNA, complete cds.	4e-09	3875371	(Z50948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f... >gi\|3878699\|gnl\|PID\|e1351700 possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f...	3e-06
1146	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-09	2494337	ENDO-1,4-BETA-XYLANASE PRECURSOR sp.]	4.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					UDP-	
1147	U20554	Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.	2e-09	2499087	GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor [Drosophila melanogaster]	4e-24
1148	Z56162	H.sapiens CpG DNA, clone 91c9, forward read cpg91c9.ft1a .	1e-09	<NONE>	<NONE>	<NONE>
1149	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-09	1002424	(U25739) YSPL-1 form 1 [Mus musculus]	8.9
1150	M85276	Homo sapiens NKG5 gene, complete cds.	1e-09	2315436	(AF016447) No definition line found [Caenorhabditis elegans]	8.3
1151	M94065	Human dihydroorotate dehydrogenase mRNA, 3' end.	1e-09	3892656	(AB014464) MGC-24v [Mus musculus]	6.2
1152	AJ131895	Homo sapiens genomic CAG repeat element, clone 60o2(250)	5e-10	<NONE>	<NONE>	<NONE>
1153	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-10	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7.9
1154	AJ224442	Homo sapiens mRNA for putative methyltransferase	5e-10	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.15
1155	AJ010230	Homo sapiens RET finger protein-like 1 antisense transcript, partial	5e-10	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.006
1156	AF111116	Homo sapiens silencer of death domains (SODD) mRNA, complete cds	5e-10	4160014	(AF111116) silencer of death domains [Homo sapiens]	2e-08
1157	Z97017	Homo sapiens mRNA for hypothetical protein	4e-10	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens type II				
1158	AF001298	integral membrane protein	4e-10	<NONE>	<NONE>	<NONE>
1159	Y11395	H.sapiens mRNA for p40	2e-10	1000340	(U34384) CheW [Borrelia burgdorferi]	2.4
1160	U41096	Human non-coding sequence upstream from DOC-2 gene on chromosome 5	2e-10	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.28
1161	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	6e-11	<NONE>	<NONE>	<NONE>
1162	Z36111	S.cerevisiae chromosome II reading frame ORF YBR242w	6e-11	2213560	(Z97052) hypothetical protein	3e-27
1163	D89174	Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1004	6e-11	3879758	(Z80220) Similarity to yeast protein TREMBL ID E246895); cDNA EST EMBL:T00018 comes from this gene; cDNA EST EMBL:C13908 comes from this gene; cDNA EST EMBL:C11656 comes from this gene; cDNA EST yk234a5.3 comes from this ge...	4e-30
1164	Z95437	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	5e-11	<NONE>	<NONE>	<NONE>
1165	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	5e-11	3886065	(AF106581) contains similarity to C4-type zinc fingers	4.9
1166	X56997	Human UbA52 gene coding for ubiquitin-52 amino acid fusion protein	2e-11	<NONE>	<NONE>	<NONE>
1167	AF086253	Homo sapiens full length insert cDNA clone ZD40G12	2e-11	2134780	apoptosis inhibitor IAP homolog - human	3.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1168	AB018314	Homo sapiens mRNA for KIAA0771 protein, partial cds	2e-11	3024343	P53-BINDING PROTEIN 53BP2 Bbp/53BP2 [Homo sapiens]	2e-11
1169	Z74972	S.cerevisiae chromosome XV reading frame ORF YOR064c	2e-11	3041855	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	2e-40
1170	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	7e-12	<NONE>	<NONE>	<NONE>
1171	X77738	H.sapiens red cell anion exchanger (EPB3, AE1, Band 3) gene, 3' region	7e-12	2135416	hypothetical protein - human >gi\|288145	0.012
1172	S61977	medium-chain acyl-CoA dehydrogenase {exon 10, intron 10} [human, Genomic, 1407 nt]	6e-12	113666	!!!! ALU CLASS A WARNING ENTRY !!!!	0.100
1173	X66285	M.musculus DNA for HC1 locus	6e-12	854065	(X83413) U88 [Human herpesvirus 6]	2e-06
1174	S78744	protein S=activated protein C cofactor [rats, liver, mRNA, 3315 nt]	6e-12	2338292	(AF009243) proline-rich Gla protein 2 [Homo sapiens]	3e-10
1175	X58474	Bovine OXT gene for oxytocin, 5' noncoding region	2e-12	1296429	(L77967) small proline-rich protein with paired repeat	4.1
1176	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.rt1a .	2e-12	2935221	(AF030154) pVII [bovine adenovirus type 3]	2.8
1177	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.rt1a .	2e-12	2708659	(AF037440) putative 26 kDa protein [Edwardsiella ictaluri]	2.8
1178	Z19543	M.musculus h2-calponin cDNA	2e-12	2497945	BETA SCRUIN >gi\|1015535 (Z47541) beta scruin [Limulus polyphemus]	2e-04

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		erythropoietin				
1179	S45332	receptor [human, placental, Genomic, 8647 nt]	7e-13	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	0.074
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1181	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1182	Z59509	H.sapiens CpG DNA, clone 15a1, reverse read cpg15a1.rt1a .	2e-13	3150251	(AL023634) hypothetical protein	0.66
1183	D10170	Human CYP11B2 gene for steroid 18-hydroxylase	2e-13	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	3e-05
1184	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-13	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6e-11
1185	AJ006031	Mus musculus IHABP gene, promoter	8e-14	2132223	hypothetical protein YPL186c - yeast	1.1
1186	U34976	Human gamma-sarcoglycan mRNA, complete cds	8e-14	1054903	(U34976) gamma-sarcoglycan [Homo sapiens] >gi\|4239660 sapiens]	0.034
1187	D30647	Rat mRNA for very-long-chain Acyl-CoA dehydrogenase, complete cds	8e-14	3183512	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (VLCAD) >gi\|2388724 (AF017176) very-long-chain acyl-CoA dehydrogenase [Mus musculus]	8e-23
1188	Z63247	H.sapiens CpG DNA, clone 7g4, forward read cpg7g4.f1a .	6e-14	86285	histone H1.01 - chicken	6.8
1189	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds.	3e-14	2134436	zinc finger protein - chicken (fragment)	4e-10
1190	M26219	African green monkey origin of replication	2e-14	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1191	AF100694	Pontin52 mRNA, complete cds	2e-14	4235641	(AF119040) NL0D [Lycopersicon esculentum]	0.65
1192	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-14	3043728	(AB011174) KIAA0602 protein [Homo sapiens]	0.28
1193	AJ005866	Homo sapiens mRNA for putative Sqv-7-like protein, partial	2e-14	4008517	(AJ005866) Sqv-7-like protein [Homo sapiens]	0.004
1194	U32709	Haemophilus influenzae Rd section 24 of 163 of the complete genome	2e-14	3861056	(AJ235272) POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (pnp) [Rickettsia prowazekii]	6e-28
1195	AF073485	Homo sapiens MHC class I-related protein MR1 precursor (MR1) gene, partial cds	8e-15	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1.0
1196	AF052135	Homo sapiens clone 23625 mRNA sequence	8e-15	4098124	(U73522) AMSH [Homo sapiens]	8e-14
1197	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1198	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	1.7
1199	Z75104	S.cerevisiae chromosome XV reading frame ORF YOR196c	3e-15	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	1e-15

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U42833) coded for by C.	
1200	X70052	S.cerevisiae sof1 gene	3e-15	1125754	elegans cDNA cm16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]	3e-29
1201	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	<NONE>	<NONE>	<NONE>
1202	M92295	Gorilla gorilla gamma 1 and gamma-2 globin genes, complete cds.	1e-15	284078	hypothetical protein 2 - human >gi\|182220	7.4
1203	L34587	Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit mRNA, complete cds. > :: gb\|AR022286\|AR022286 Sequence 7 from patent US 5792634	9e-16	<NONE>	<NONE>	<NONE>
1204	D83649	Xenopus laevis mRNA for xSox7 protein, complete cds	8e-16	2447043	(D83649) xSox7 protein [Xenopus laevis]	4e-06
1205	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23; complete sequence [Homo sapiens]	3e-16	<NONE>	<NONE>	<NONE>
1206	J03626	Human UMP synthase mRNA, complete cds.	3e-16	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.65
1207	J00083	Human Alu family interspersed repeat; clone BLUR11.	3e-16	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	4e-06
1208	U70674	Mus musculus m-Numb (m-nb) mRNA, complete cds	1e-16	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1209	U66619	Human SWI/SNF complex 60 KDa subunit (BAF60c) mRNA, complete cds	1e-16	1549247	(U66619) SWI/SNF complex 60 KDa subunit [Homo sapiens]	0.003
1210	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	1e-16	1658503	(U75467) Atu [Drosophila melanogaster]	5e-32
1211	M72709	Human alternative splicing factor mRNA, complete cds.	3e-17	<NONE>	<NONE>	<NONE>
1212	U26556	Human ferritin H (FTHL13) pseudogene.	3e-17	<NONE>	<NONE>	<NONE>
1213	D32064	Human gene for 2-oxoglutarate dehydrogenase, complete cds	3e-17	2088843	(AF003386) F59E12.9 gene product [Caenorhabditis elegans]	0.12
1214	M76364	Human (Papua New Guinean) Mitochondrial DNA control region, sequence 131.	3e-17	114009	APAG PROTEIN >gi\|72927\|pir\|\|BVECAG apaG protein - Escherichia coli >gi\|40918 (X04711) URF hypothetical protein [Escherichia coli]	0.006
1215	AF017466	Homo sapiens genomic sequence from subtelomeric region of chromosome 4q	1e-17	3947985	(U78948) MADS-box protein 2 [Malus domestica]	4.1
1216	AF004876	Homo sapiens 54TMp (54tm) mRNA, complete cds	1e-17	4101574	(AF004876) 54TMp [Homo sapiens]	0.006
1217	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-18	<NONE>	<NONE>	<NONE>
1218	AF086758	Rattus norvegicus Na-K-2Cl cotransporter	4e-18	3892703	(AL033545) putative glycine-rich protein [Arabidopsis thaliana]	0.30
1219	AF020089	Homo sapiens PEN11B mRNA, complete cds	4e-18	2642493	(AF023910) DNA topoisomerase I [Physarum polycephalum]	0.083
1220	X82333	H.sapiens IRLB gene (exon1-3)	4e-18	106837	irlB protein - human (fragment) >gi\|33969	2e-11

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1221	AB002383	Human mRNA for KIAA0385 gene, complete cds	4e-18	3228540	(AF060181) zinc finger protein [Homo sapiens]	6e-25
1222	X98485	P.vivax PV14 gene	1e-18	<NONE>	<NONE>	<NONE>
1223	Z79057	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA21E8	1e-18	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
1224	L01457	Homo sapiens (clone JH4B1) PM-scl autoantigen mRNA, complete cds.	1e-18	346287	nucleolar 100K polymyositis-scleroderma protein - human >gi\|35555 (X66113) PM/Scl 100kD nucleolar protein [Homo sapiens]	0.001
1225	L02897	Dog nonerythroid beta-spectrin mRNA, 3' end.	4e-19	3493358	(AB017037) nonstructural protein precursor [Himetobi P virus]	0.12
1226	AB012162	Homo sapiens mRNA for APCL protein, complete cds	4e-19	3894265	(AB012162) APCL protein [Homo sapiens]	0.002
1227	AB011093	Homo sapiens mRNA for KIAA0521 protein, partial cds	4e-19	3043566	(AB011093) KIAA0521 protein [Homo sapiens]	9e-09
1228	X78454	X.laevis AB21 mRNA for RPD3 homologue	4e-19	3023945	HISTONE DEACETYLASE (HD) thaliana]	5e-34
1229	U88895	Human endogenous retrovirus H D1 leader region/integrase-derived ORF1, ORF2, and putative envelope protein mRNA, complete cds	2e-19	59977	(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	1e-04
1230	U34377	Human tyrosine kinase TXK (txk) gene, exon 13.	1e-19	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-05
1231	X72966	M.musculus rab3A gene	1e-19	2408076	(Z99167) putative peroxisomal organisation and biogenesis protein [Schizosaccharomyces pombe]	2e-09
1232	AB007953	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484	4e-20	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AB001535) similar to	
1233	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-20	3928756	C.elegans hypothetical protein CET01H8.1,CEC05C12.3,CEF5 4D1.5. similar to trp and trp-like proteins [Homo sapiens]	1e-07
1234	X82126	H.sapiens HOK-2 gene, exon 2	2e-20	2137269	DNA-binding protein - mouse >gi\|437444	1e-19
1235	AF093684	Luciferase reporter vector pXP2 *SA, complete sequence	5e-21	2773363	(AF041382) microtubule binding protein D-CLIP-190	5.5
1236	J05272	Human IMP dehydrogenase type 1 mRNA complete cds.	5e-21	124417	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (IMP DEHYDROGENASE 1) (IMPDH-I) (IMPD 1) I - human	2e-04
1237	D86997	Human (lambda) DNA for immunoglobulin light chain	5e-21	3878261	(Z75712) Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST EMBL:Z14470 comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST yk482d4.5 comes from this gene [Caenorhabditis elegans]	6e-46
1238	Z79865	H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 302f3, forward read 302f3.f	2e-21	2739037	(AF024614) ADAM 10 [Caenorhabditis elegans] Zinc-binding metalloprotease domain; cDNA EST CEMSA42F comes from this gene; cDNA EST yk218f3.3 comes from this gene; cDNA EST yk443d9.3 comes from this gene; cDNA EST yk443d9.5 comes from this gene; cDNA...	2.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AL008985) similar to tammm B, cDNA EST yk450d8.5 comes	
1239	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-22	3924779	from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi\|3924881\|gnl\|PID\|e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.35
1240	U67824	Human primary Alu transcript	6e-22	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	5e-07
1241	AF070636	Homo sapiens clone 24686 mRNA sequence	2e-22	98710	fatty-acid synthase (EC 2.3.1.85) - Brevibacterium ammoniagenes	2.5
1242	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-22	4185939	(Y17832) pol protein [Human endogenous retrovirus K]	0.29
1243	M61835	Human lactase phlorizin hydrolase (LCT) gene, exon 2.	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.006
1244	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	1350828	RABPHILIN-3A >gi\|477100\|pir\|\|A48097 rabphilin-3A - bovine >gi\|285646\|gnl\|PID\|d1003285	0.14
1245	AF074985	Homo sapiens full length insert cDNA YH73H06	8e-24	3170548	(AF056116) unknown [Fugu rubripes]	0.24
1246	D14878	Human mRNA for protein D123, complete cds	7e-24	<NONE>	<NONE>	<NONE>
1247	D16917	Human HepG2 3' region cDNA, clone hmd3d07	6e-24	1397345	(U61955) contains multiple region of strong similarity to C2H2-type zinc fingers (PS:PS00028) [Caenorhabditis elegans]	2.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1248	Z69654	sequence from cosmid L98A6, Huntington's Disease Region, chromosome 4p16.3.	3e-24	4240566	(AF123462) neurexin III [Homo sapiens]	4.5
1249	AB007914	Homo sapiens mRNA for KIAA0445 protein, complete cds	2e-24	3885949	(AF095568) amelogenin [Paleosuchus palpebrosus]	3.2
1250	AF088072	Homo sapiens full length insert cDNA clone ZD93D10	2e-24	323091	immunodominant microneme protein Etp100 - Eimeria tenella >gi\|2707733 (AF032905) microneme protein precursor Etmic-1 [Eimeria tenella]	0.34
1251	AF069489	Homo sapiens cAMP specific phosphodiesterase 4A variant pde46 (PDE4A) gene, exons 2 through 13 and alternative splice exons 3a, 6a, 6b, and 9a	2e-24	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	1e-05
1252	Y12853	Homo sapiens P2X7 gene, exon 4-8	9e-25	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-05
1253	M27830	Human 28S ribosomal RNA gene, complete cds.	8e-25	<NONE>	<NONE>	<NONE>
1254	AB007953	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484	8e-25	<NONE>	<NONE>	<NONE>
1255	Z60212	H.sapiens CpG DNA, clone 195c8, forward read cpg195c8.ft1a .	8e-25	158154	(M81959) POU domain protein [Drosophila melanogaster]	3.3
1256	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1257	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1258	Y12851	Homo sapiens P2X7 gene, exon 1 and joined CDS	2e-25	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus Tera				
1259	U64033	(Tera) mRNA, complete cds	9e-26	<NONE>	<NONE>	<NONE>
1260	U19181	Rattus norvegicus Rabin3 mRNA, complete cds.	9e-26	624225	(U19181) Rabin3 [Rattus norvegicus]	1e-13
1261	AF020788	Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds	9e-26	3915881	SEL-10 PROTEIN Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:D27698 comes from this gene; cDNA EST EMBL:D32793 comes from this gene; cDNA EST EMBL:D33271 comes from this gen...	7e-32
1262	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	8e-26	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	0.045
1263	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-26	3878629	(Z93385) predicted using Genefinder; Similarity to B.subtilis GTP-binding protein	2e-10
1264	X91195	H.sapiens SOM172 mRNA	1e-26	<NONE>	<NONE>	<NONE>
1265	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-26	1360637	(X95995) ENBP1 [Vicia sativa]	3.1
1266	L08237	Human MG21 mRNA, partial cds.	1e-26	950411	(L08237) located at OATL1 [Homo sapiens]	9e-09
1267	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	3881080	(AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8....	0.001
1268	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-27	1731324	HYPOTHETICAL PROTEIN >gi\|166306	4.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1269	X89211	H.sapiens DNA for endogenous retroviral like element	8e-27	2065209	(Y12713) Gag polyprotein [Mus musculus]	0.005
1270	U73166	Homo sapiens cosmid clone LUCA15 from 3p21.3, complete sequence [Homo sapiens]	3e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4e-04
1271	D78255	Mouse mRNA for PAP-1, complete cds	3e-27	1850098	(D78255) PAP-1 [Mus musculus]	2e-10
1272	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.39
1273	AB015202	Homo sapiens gene for hippocalcin, exon 2, 3 and complete cds	1e-27	3877698	(Z83318) predicted using Genefinder; cDNA EST yk369e7.5 comes from this gene [Caenorhabditis elegans]	0.37
1274	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.19
1275	Z29336	H.sapiens gene for Cu/Zn-superoxide dismutase	1e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	6e-05
1276	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	9.2
1277	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.054
1278	AB001636	Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds	4e-28	3913425	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi\|2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]	3e-22
1279	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.066

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
1280	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454	region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	4e-05
1281	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1282	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1283	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1284	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1285	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1286	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1287	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi\|11663	3.0
1288	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi\|11663	1.8
1289	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.50
1290	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.087
1291	Z63029	H.sapiens CpG DNA, clone 77b3, forward read cpg77b3.ft1a .	1e-28	2493240	HYPOTHETICAL 29.3 KD PROTEIN pseudotsugata nuclear polyhedrosis virus]	0.014

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DEHYDRIN DHN3	
1292	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	>gi\|100035\|pir\|\|S18139 dehydrin DHN3 - garden pea >gi\|20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.010
1293	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.007
1294	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1295	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	3e-04
1296	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1297	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	3e-05
1298	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb\|Z34465 from Zea mays. [Arabidopsis thaliana]	2e-05
1299	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					kinetoplast-associated protein -	
1300	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	320919	Trypanosoma cruzi >gi\|162142 (M25364) kinetoplast-associated protein	1e-07
1301	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	9e-08
1302	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1303	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	9e-10
1304	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	4e-10
1305	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	9e-11
1306	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	6e-11

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1307	AF100694	Pontin52 mRNA, complete cds	4e-29	<NONE>	<NONE>	<NONE>
1308	AF079529	Homo sapiens cAMP-specific phosphodiesterase 8B	4e-29	<NONE>	<NONE>	<NONE>
1309	X93334	H.sapiens mitochondrial DNA, complete genome	4e-29	116977	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - human mitochondrion (SGC1) >gi\|13006 (V00662) cytochrome oxidase I [Homo sapiens] >gi\|506829 (J01415) cytochrome oxidase subunit 1 [Homo sapiens] sapiens]	3e-09
1310	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	4e-29	2738915	(AF020760) serine protease [Homo sapiens]	8e-12
1311	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	4e-29	2072294	(U95097) mitotic phosphoprotein 43 [Xenopus laevis]	1e-25
1312	L32162	Homo sapiens transcription factor mRNA, 5' end.	2e-29	2501706	RENAL TRANSCRIPTION FACTOR KID-1 finger protein [Mus musculus]	8e-15
1313	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	4056454	(AC005990) Contains repeated region with similarity to gb\|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb\|Z34165 and gb\|Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1314	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi\|416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	1e-05
1315	U50839	Homo sapiens g16 protein (g16) mRNA, complete cds	1e-29	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	6e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					intercellular adhesion molecule	
1316	X69711	H. sapiens mRNA for ICAM-R	5e-30	299356	3, ICAM-3=lymphocyte function-associated antigen 1 counter-receptor homolog [human, tonsil, Peptide Partial, 518 aa]	3e-08
1317	AF010227	Homo sapiens receptor-associated coactivator 3	5e-30	2331250	(AF012108) Amplified in Breast Cancer [Homo sapiens]	8e-09
1318	AF086395	Homo sapiens full length insert cDNA clone ZD75C01	2e-30	3861241	(AJ235273) CELL SURFACE ANTIGEN (sca5)	4.2
1319	M27830	Human 28S ribosomal RNA gene, complete cds.	2e-30	1730522	PHOSPHOGLYCERATE KINASE 2.7.2.3) - Pyrococcus woesei >gi\|1054832 (X73527) phosphoglycerate kinase [Pyrococcus woesei]	3.8
1320	M79307	Mouse GTP-binding protein (Rab17) mRNA sequence.	2e-30	464564	RAS-RELATED PROTEIN RAB-17 Rab17 - mouse (fragment) >gi\|297157 (X70804) rab17 [Mus musculus]	9e-11
1321	AL022168	Human DNA sequence from clone U247E12 on chromosome Xq22-23, complete sequence [Homo sapiens]	1e-30	2072967	(U93570) putative p150 [Homo sapiens]	3e-11
1322	X85124	M.musculus pacsin gene	1e-30	2217964	(Z50798) p52 [Gallus gallus]	1e-34
1323	U37408	Homo sapiens phosphoprotein CtBP mRNA, complete cds	5e-31	74518	structural polyprotein - Venezuelan equine encephalitis virus (strain TRD) >gi\|323710 (J04332) poly-envelope protein [Venezuelan equine encephalitis virus]	1.1
1324	L04193	Human lens membrane protein (mp19) gene, exon 11.	2e-31	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7e-07
1325	M11167	Human 28S ribosomal RNA gene.	6e-32	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1326	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds	2e-32	<NONE>	<NONE>	<NONE>
1327	J03060	Human glucocerebrosidase pseudogene, complete cds	2e-32	2144479	glucosylceramidase (EC 3.2.1.45) precursor - human	1e-05
1328	U33053	Human lipid-activated protein kinase PRK1 mRNA, complete cds	7e-33	2137689	protein kinase (EC 2.7.1.37) - mouse	1e-14
1329	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj\|E02629\|E02629 DNA of human polypeptide chain elongation factor-1 alpha	6e-33	<NONE>	<NONE>	<NONE>
1330	L40396	Homo sapiens (clone s22i71) mRNA fragment	6e-33	124235	INTERMEDIATE FILAMENT PROTEIN B protein B - common roundworm	1.00
1331	Z72813	S.cerevisiae chromosome VII reading frame ORF YGR028w	6e-33	1709135	MSP1 PROTEIN HOMOLOG Yeast MSP1 protein (TAT-binding homolog 4)	8e-50
1332	AB007941	Homo sapiens mRNA for KIAA0472 protein, partial cds	2e-33	1150834	(U42471) Wiscott-Aldrich Syndrome protein homolog [Mus musculus]	2.0
1333	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	2e-34	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	6e-15
1334	D14657	Human mRNA for KIAA0101 gene, complete cds	7e-35	<NONE>	<NONE>	<NONE>
1335	X69910	H.sapiens p63 mRNA for transmembrane protein	7e-35	2136323	trithorax homolog HTX - human (fragment) homolog=MLL {alternative splicing, clone 14p-18B}	0.94

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1336	AF053455	tetraspan TM4SF (TSPAN-5) gene, complete cds	7e-35	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	1e-25
1337	X58374	D.melanogaster crn mRNA	3e-35	117478	CROOKED NECK PROTEIN	6e-41
1338	AF086492	Homo sapiens full length insert cDNA clone ZD95D11	9e-36	2909809	(AF031328) aminoglycoside 6'-N-acetyltransferase It	1.9
1339	Z96223	H.sapiens telomeric DNA sequence, clone 12PTEL120, read 12PTELOO120.seq	3e-36	2408068	(Z99165) hypothetical protein	0.61
1340	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	1e-36	1362793	emopamil-binding protein - human >gi\|780263	5e-11
1341	U57847	Human ribosomal protein S27 mRNA, complete cds. end similar to similar to metallopanstimulin 1 > :: gb\|AA316327\|AA316327 EST188061 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to metallopanstimulin 1	3e-37	1171014	40S RIBOSOMAL PROTEIN S27 growth factor-inducible zinc finger protein MPS-1 - human >gi\|431319 (L19739) metallopanstimulin [Homo sapiens] >gi\|1373421 (U57847) ribosomal protein S27	1.4
1342	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-37	3123027	70 KD WD-REPEAT TUMOR-SPECIFIC ANTIGEN >gi\|2505957\|gnl\|PID\|e353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	2e-15
1343	AF084205	Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds	3e-37	3452473	(AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	5e-47
1344	X78604	R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5	1e-37	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1345	AJ236644	Homo sapiens chromosome 22 CpG island DNA, genomic Mse1 fragment, clone 22CGIB49A3 , complete read	1e-37	2239219	(Z97210) hypothetical protein	6e-05
1346	U09367	Human zinc finger protein ZNF136	4e-39	2137269	DNA-binding protein - mouse >gi\|437444	7e-23
1347	Z69649	Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, chromosome 4p16.3 contains Huntington Disease (HD) gene.	3e-39	3096918	(AL023094) putative cyclase associated protein CAP [Arabidopsis thaliana]	5.6
1348	AF065389	Homo sapiens tetraspan NET-4 mRNA, complete cds	1e-39	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	6e-29
1349	AF038172	Homo sapiens clone 23923 mRNA sequence	1e-40	1813464	(U60883) CapC [Bacillus firmus]	2.8
1350	Z83095	H.sapiens Fanconi anaemia group A gene, exons 39, 40, 41, 42 and 43	1e-40	2137870	zinc finger protein - mouse (fragment)	3e-23
1351	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	1e-40	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	6e-61
1352	AF070567	Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds	4e-41	3133087	(Y15718) dystrobrevin B DTN-B2 [Homo sapiens]	7e-13
1353	AF006088	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) mRNA, complete cds	2e-41	3121767	ARP2/3 COMPLEX 16 KD SUBUNIT	3e-36
1354	X69942	M.musculus mRNA of enhancer-trap-locus 1	6e-42	2291152	(AF016418) No definition line found [Caenorhabditis elegans]	6.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1355	X87838	H.sapiens mRNA for beta-catenin	5e-42	1373019	(U28811) cysteine-rich fibroblast growth factor receptor	8e-05
1356	AB018268	Homo sapiens mRNA for KIAA0725 protein, partial cds	5e-42	3882171	(AB018268) KIAA0725 protein [Homo sapiens]	2e-33
1357	M84424	Human cathepsin E (CTSE) gene, exon 9 and complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1358	U80776	Human EST clone NIB1543 mariner transposon Hsmar1 orf gene, complete cds	2e-42	2231380	(U80776) orf; encodes putative chimeric protein with SET domain in N-terminus with similarity to several other human, Drosophila, nematode and yeast proteins [Homo sapiens]	3e-11
1359	U55184	Human G protein Golf alpha gene, exon 12 and complete cds	2e-42	3165531	(AF067608) No definition line found [Caenorhabditis elegans]	1e-16
1360	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence [Homo sapiens]	6e-43	2978255	(AB007407) myeloid zinc finger protein-2 [Mus musculus]	2.3
1361	AB018284	Homo sapiens mRNA for KIAA0741 protein, complete cds	5e-43	<NONE>	<NONE>	<NONE>
1362	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	5e-43	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	1e-07
1363	M93651	Human set gene, complete cds.	2e-43	<NONE>	<NONE>	<NONE>
1364	Z47087	H.sapiens mRNA for RNA polymerase II elongation factor-like protein.	2e-43	1872514	(U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens] >gi\|2361031 (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens]	7.2
1365	U27197	Drosophila melanogaster pelota (pelo) mRNA, complete cds	2e-43	1352736	PELOTA PROTEIN >gi\|973224 (U27197) pelota [Drosophila melanogaster]	1e-46

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RRP5 PROTEIN HOMOLOG	
1366	D80007	Human mRNA for KIAA0185 gene, partial cds	6e-44	2498864	(KIAA0185) hypothetical protein YM9959.11C of S.cerevisiae. [Homo sapiens]	6e-09
1367	AF005039	Homo sapiens secretory carrier membrane protein (SCAMP3) mRNA, complete cds	6e-44	2232243	(AF005039) secretory carrier membrane protein [Homo sapiens]	2e-09
1368	X68101	R.norvegicus trg mRNA	2e-44	550420	(X68101) trg gene product [Rattus norvegicus]	1e-37
1369	AF044206	Homo sapiens cyclooxygenase (COX-2) gene, promoter and exon 1	2e-45	2072953	(U93565) putative p150 [Homo sapiens]	5e-06
1370	L48708	Homo sapiens faciogenital dysplasia (FGD1) gene, 5' end of intron 17	8e-46	<NONE>	<NONE>	<NONE>
1371	X15822	Human COX VIIa-L mRNA for liver-specific cytochrome c oxidase (EC 1.9.3.1.)	3e-46	117121	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR >gi\|2144370\|pir\|\|OSHU7L cytochrome-c oxidase (EC 1.9.3.1) chain VIIa precursor, hepatic - human >gi\|30147 (X15822) precursor (AA -23 to 60) [Homo sapiens]	5e-13
1372	U47323	Mus musculus stromal cell protein mRNA, complete cds	3e-46	1493833	(U47323) stromal cell protein [Mus musculus]	1e-48
1373	AF059524	Homo sapiens reticulon gene family protein	7e-47	1731169	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME II >gi\|861264 (U28738) coded for by C. elegans cDNA yk8h5.3; coded for by C. elegans cDNA yk8h5.5; similar to C. elegans deg-1 and mec-4 in exon 2 [Caenorhabditis elegans]	7.8
1374	AJ132583	Homo sapiens mRNA for puromycin sensitive aminopeptidase, partial	3e-47	1777519	(U39123) T cell receptor beta chain [Homo sapiens]	9.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1375	M97856	Homo sapiens histone binding protein mRNA, complete cds.	3e-47	2645327	(U83821) NADH dehydrogenase subunit 3 [Oryzomys palustris]	5.7
1376	U53220	Human retinoblastoma-related Rb2/p130 gene, 5' flanking region and partial cds	3e-47	2499225	CMP-SIALIC ACID TRANSPORTER CMP-sialic acid transporter [Cricetulus griseus]	5.3
1377	X87870	H.sapiens mRNA for hepatocyte nuclear factor 4a	1e-47	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	7.3
1378	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	3e-48	478681	limb deformity protein - chicken	0.25
1379	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-48	3122969	TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA) >gi\|281040\|pir\|\|S28499 probable zinc finger protein - rat >gi\|57504 (X59993) zinc finger protein	1e-30
1380	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	4e-49	88558	retroviral proteinase-like protein - human	6e-05
1381	AB007956	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487	1e-49	<NONE>	<NONE>	<NONE>
1382	D86987	Homo sapiens mRNA for KIAA0214 protein, complete cds	1e-49	2497944	ALPHA SCRUIN >gi\|633238 (Z38132) scruin [Limulus polyphemus] >gi\|1093326\|prf\|\|2103269A scrulin [Limulus sp.]	9.7
1383	U25826	Human transcription factor (SC1) gene, complete cds.	4e-50	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus ATP-				
1384	U46690	dependent RNA helicase mRNA, partial cds.	4e-50	1335873	(U46690) ATP-dependent RNA helicase [Mus musculus]	3e-24
1385	AF072128	Mus musculus claudin-2 mRNA, complete cds	2e-50	3335184	(AF072128) claudin-2 [Mus musculus]	4e-24
1386	AF093593	Homo sapiens snRNA activating protein complex 19kDa subunit (SNAP19) mRNA, complete cds	1e-50	3668416	(AF093593) snRNA activating protein complex 19kDa subunit [Homo sapiens]	0.003
1387	U79745	Homo sapiens monocarboxylate transporter homologue MCT6 mRNA, complete cds	1e-50	1177607	(X92485) pva1 [Plasmodium vivax]	2e-07
1388	L09647	Rattus norvegicus hepatocyte nuclear factor 3a	1e-50	404764	(L10409) fork head related protein [Mus musculus]	2e-21
1389	X61506	Mouse E46 mRNA for E46 protein	4e-51	114909	BRAIN PROTEIN E46	1e-20
1390	M33387	Human debrisoquine 4-hydroxylase (CYP2D8P) and	1e-51	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	5e-15
1391	AF019767	Homo sapiens zinc finger protein (ZPR1) mRNA, complete cds	4e-52	961507	(D63788) anchor protein, LCM	5.9
1392	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	2e-52	<NONE>	<NONE>	<NONE>
1393	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-52	3878637	(Z49128) weak similarity with SINR protein (Swiss Prot accession number P06533); cDNA EST EMBL:T00631 comes from this gene; cDNA EST yk293d10.5 comes from this gene [Caenorhabditis elegans]	8.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					beta-globin DNA-binding	
1394	Z57647	H.sapiens CpG DNA, clone 189a6, forward read cpg189a6.ft1a .	2e-52	111187	protein B1, transcription factor PU.1 - mouse >gi\|200586 (M32370) PU.1 protein [Mus musculus] >gi\|200972 (M38252) transcription factor Pu.1 [Mus musculus]	5.8
1395	L13738	Human activated p21cdc42Hs kinase (ack) mRNA, complete cds.	2e-52	2921447	(AF037260) non-receptor protein tyrosine kinase Ack [Mus musculus]	7e-23
1396	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	7e-53	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	1e-16
1397	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	6e-53	3914807	DNA-DIRECTED RNA POLYMERASE I 40 KD POLYPEPTIDE (RPA40) (RPA39) >gi\|2266929 (AF008442) RNA polymerase I subunit hRPA39 [Homo sapiens]	4e-19
1398	AF104670	Homo sapiens cell cycle protein (PA2G4) gene, exons 6 through 13, and complete cds	2e-53	<NONE>	<NONE>	<NONE>
1399	S60754	{VNTR locus DXZ4, hypervariable tandem repeat cluster} [human, Genomic, 2991 nt] > :: gb\|L07935\|HUMVNTRA Homo sapiens microsatellite VNTR DNA sequence.	2e-53	1209669	(U38810) CAGR1 [Homo sapiens] >gi\|3098420 (AF040945) homeotic regulator homolog MAB21 [Mus musculus]	4.6
1400	D86972	Human mRNA for KIAA0218 gene, complete cds	1e-53	3426041	(AC005168) unknown protein [Arabidopsis thaliana]	9.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1401	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic Mse1 fragment, clone 22CGIB49E6 , complete read	7e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.30
1402	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic Mse1 fragment, clone 22CGIB49E6 , complete read	6e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.28
1403	M37583	Human histone (H2A.Z) mRNA, complete cds.	6e-54	70711	histone H2A.F, embryonic - chicken	2e-16
1404	AJ009947	Homo sapiens mRNA for putative ATPase, partial	6e-54	3550295	(AJ009947) putative ATPase [Homo sapiens]	3e-18
1405	Y08459	B.taurus mRNA for novel cytoplasmic protein	2e-54	<NONE>	<NONE>	<NONE>
1406	AF042384	Homo sapiens BC-2 protein mRNA, complete cds	2e-54	2828147	(AF042384) BC-2 protein [Homo sapiens]	2e-14
1407	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	8e-55	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	2e-17
1408	AF005355	Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds	7e-55	3253159	(AF005355) translation initiation factor eIF2C	3e-53
1409	AF008442	Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20
1410	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for				
1411	X08004	Rap1B protein > :: emb\|A08693\|A08693 H.sapiens rap1b cDNA	2e-55	539995	transforming protein rap1b - rat (strain Copenhagen)	2e-18
1412	AF010403	Homo sapiens ALR mRNA, complete cds	2e-55	2358285	(AF010403) ALR [Homo sapiens]	1e-49
1413	M77016	Human tropomodulin mRNA, complete cds.	8e-56	262249	(S52010) orf1 5' of EpoR [mice, Peptide, 85 aa] [Mus sp.]	0.027
1414	AB020633	Homo sapiens mRNA for KIAA0826 protein, partial cds	2e-56	<NONE>	<NONE>	<NONE>
1415	X87489	H.sapiens genomic DNA (chromosome 3; clone NL1243D)	2e-56	1814029	(U84501) cuticle collagen [Caenorhabditis briggsae]	0.038
1416	AB007893	Homo sapiens KIAA0433 mRNA, partial cds	2e-56	2887437	(AB007893) KIAA0433 [Homo sapiens]	9e-21
1417	X78925	H.sapiens HZF2 mRNA for zinc finger protein	1e-56	3342002	(AF054180) hematopoietic cell derived zinc finger protein [Homo sapiens]	2e-21
1418	Z56281	H.sapiens mRNA for interferon regulatory factor 3	9e-57	2497442	INTERFERON REGULATORY FACTOR 3 factor 3 [Homo sapiens]	2e-21
1419	U78772	Homo sapiens nuclear VCP-like protein NVLp.1	8e-57	2406565	(U68140) nuclear VCP-like protein NVLp.2 [Homo sapiens]	5e-20
1420	D79994	Human mRNA for KIAA0172 gene, partial cds	3e-57	1136404	(D79994) similar to ankyrin of Chromatium vinosum. [Homo sapiens]	9e-38
1421	AB002342	Human mRNA for KIAA0344 gene, complete cds	1e-57	2224629	(AB002342) KIAA0344 [Homo sapiens]	4e-20
1422	L19437	Human transaldolase mRNA containing transposable element, complete cds	1e-57	1553119	(U63159) transaldolase [Mus musculus]	2e-20
1423	D17532	Human mRNA for RCK, complete cds	9e-58	129376	PROBABLE ATP-DEPENDENT RNA HELICASE P54 (ONCOGENE RCK) (DEAD BOX PROTEIN 6)	1e-10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1424	X79568	H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	1e-22
1425	X79568	H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	9e-23
1426	AB012295	Homo sapiens HKE1.5 mRNA for GDS-related protein, complete cds	7e-58	2648021	(Z97184) RGL2 [Homo sapiens]	9e-19
1427	AF086040	Homo sapiens full length insert cDNA clone YX52E07	1e-58	543222	glutamine (Q)-rich factor 1, QRF-1 - mouse factor 1, QRF-1 [mice, B-cell leukemia, BCL1, Peptide Partial, 84 aa]	3e-36
1428	AB018195	Homo sapiens ca xi mRNA for carbonic anhydrase-related protein XI, complete cds	4e-59	<NONE>	<NONE>	<NONE>
1429	AF071777	Mus musculus IRE1 (Ire1) mRNA, complete cds	4e-59	3766209	(AF071777) IRE1 [Mus musculus]	7e-28
1430	AB000462	Homo sapiens mRNA for SH3 binding protein, complete cds, clone:RES4-23A	3e-59	<NONE>	<NONE>	<NONE>
1431	AF038172	Homo sapiens clone 23923 mRNA sequence	3e-59	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	1.3
1432	Z84812	Human DNA sequence from phage pTEL from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs	1e-59	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	2.5
1433	U36484	Human laminin-binding protein gene, partial cds, and E2 small nucleolar RNA gene, complete sequence	1e-59	226005	protein 40kD [Mus musculus]	7e-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DUAL SPECIFICITY	
1434	L11285	Homosapiens ERK activator kinase (MEK2) mRNA.	1e-59	2499630	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 (MAP KINASE KINASE 2) (MAPKK 2) kinase type 2 [Gallus gallus]	3e-21
1435	AF086555	Homo sapiens full length insert cDNA clone ZE14E04	4e-60	3287674	(AC005239) F23149_1 [Homo sapiens]	2e-04
1436	M24766	Human (clone pHAIV2-12) alpha-2 collagen type IV	4e-60	29551	(X05610) alpha (2) chain [Homo sapiens]	6e-15
1437	X65550	H.sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67	4e-60	1170654	ANTIGEN KI-67 >gi\|539555\|pir\|\|A48666 cell proliferation antigen Ki-67, long form - human Ki-67 [Homo sapiens]	3e-15
1438	M27319	Human calmodulin mRNA, complete cds.	4e-60	1345451	(X05949) Calmodulin (AA 2 - 59) (449 is 1st base in codon) [Drosophila melanogaster]	7e-20
1439	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	3e-60	62133	(X06172) put. 134 kD protein (AA 1 - 1187); put. replicase	7.4
1440	AB002383	Human mRNA for KIAA0385 gene, complete cds	1e-60	1001548	(D64000) hypothetical protein	4.4
1441	AF070614	Homo sapiens clone 24732 unknown mRNA, partial cds	2e-61	3283879	(AF070614) unknown [Homo sapiens]	3e-17
1442	AB002326	Human mRNA for KIAA0328 gene, partial cds	6e-62	547891	MICROTUBULE-ASSOCIATED PROTEIN 4 microtubule-associated protein-U [Bos taurus]	5.6
1443	AF086471	Homo sapiens full length insert cDNA clone ZD88A01	5e-62	<NONE>	<NONE>	<NONE>
1444	AB002311	Human mRNA for KIAA0313 gene, complete cds	2e-62	2506357	2,3-DIHYDROXYPHENYLPROPIONATE 1,2-DIOXYGENASE >gi\|1657544 (U73857) similar to mcpI gene (catechol 2,3-dioxygenase) of A. eutrophus 3-(2,3-dihydroxyphenylpropionate)1, 2-dioxygenase 2,3-dihydroxyphenylpropionate 1,2-dioxygenase	3.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1445	AF069737	Xenopus laevis notchless (nle) mRNA, complete cds	2e-62	3687833	(AF069737) notchless [Xenopus laevis]	1e-55
1446	AF044209	Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds	5e-63	2137603	nuclear receptor co-repressor N-CoR - mouse musculus] >gi\|1583865\|prf\|\|2121436A thyroid hormone receptor co-repressor [Mus musculus]	2e-47
1447	M69238	Human aryl hydrocarbon receptor nuclear translocator (ARNT) mRNA, complete cds.	2e-63	2702319	(AF001307) aryl hydrocarbon receptor nuclear translocator; Arnt [Homo sapiens]	5e-19
1448	X80497	H.sapiens PHKLA mRNA	2e-63	1170685	PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) >gi\|663010 (X80497) phosphorylase kinase phosphorylase kinase alpha subunit [Homo sapiens]	5e-22
1449	AF031141	Homo sapiens ubiquitin conjugating enzyme	2e-63	2623260	(AF031141) ubiquitin conjugating enzyme [Homo sapiens]	1e-23
1450	Z37166	H.sapiens BAT1 mRNA for nuclear RNA helicase	6e-64	2500529	PROBABLE ATP-DEPENDENT RNA HELICASE P47 >gi\|2135840\|pir\|\|I37201 nuclear RNA helicase (DEAD family) BAT1 - human >gi\|587146 (Z37166) nuclear RNA helicase (DEAD family) [Homo sapiens]	9e-24
1451	M64240	Human helix-loop-helix zipper protein (max) mRNA, complete cds. > :: gb\|I41138\|I41138 Sequence 1 from patent US 5624818 > :: gb\|I77062\|I77062 Sequence 1 from patent US 5693487	5e-64	88175	Myc-binding factor Max, short form - human	8e-22

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROCOLLAGEN-LYSINE,2-	
1452	M98252	Homo sapiens lysyl hydroxylase (partial clone 2.2 Kb LH) RNA, complete mature peptide.	2e-64	400205	OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE) lysyl hydroxylase [Homo sapiens]	7e-22
1453	U09550	Human oviductal glycoprotein mRNA, complete cds.	8e-65	2493676	OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN)	2e-11
1454	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	7e-65	423664	resiniferatoxin-binding protein RBP-26, cytosolic - rat >gi\|311660 (X67877) cytosolic resiniferatoxin binding protein RBP-26 [Rattus norvegicus] >gi\|1093373\|prf\|\|2103310A resiniferatoxin-binding protein [Rattus norvegicus]	2e-40
1455	AB018254	Homo sapiens mRNA for KIAA0711 protein, complete cds	6e-65	92298	glutamine/glutamic acid-rich protein	0.98
1456	J03607	Human 40-kDa keratin intermediate filament precursor gene.	3e-65	1070608	keratin 19, type I, cytoskeletal - human sapiens]	4e-07
1457	U65896	Human gamma-glutamyl carboxylase gene, complete cds	2e-65	<NONE>	<NONE>	<NONE>
1458	U07681	Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds.	2e-65	1708399	ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) dehydrogenase alpha chain precursor - human >gi\|706839 subunit precursor [Homo sapiens]	4e-26
1459	U88080	Human zinc finger protein (LD5-1) gene, exons 4, 5 and 6, and complete cds	2e-65	1373394	(U57796) zinc finger protein [Homo sapiens] >gi\|2306773	2e-39

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					tensin - chicken (fragment)	
1460	M96625	Gallus domesticus tensin mRNA sequence.	3e-66	2134419	>gi\|63805 (Z18529) tensin [Gallus gallus] >gi\|212755 (L06662) tensin [Gallus gallus]	1e-51
1461	U13262	Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.	1e-70	536926	(U13262) myelin gene expression factor [Mus musculus]	9e-42
1462	U64033	Mus musculus Tera (Tera) mRNA, complete cds	5e-72	1575505	(U64033) Tera [Mus musculus]	9e-34
1463	X78989	M.musculus mRNA for testin	6e-74	1351218	TESTIN 2 (TES2) [CONTAINS: TESTIN 1	8e-31
1464	U64033	Mus musculus Tera (Tera) mRNA, complete cds	2e-74	1575505	(U64033) Tera [Mus musculus]	5e-37
1465	AF057365	Canis familiaris UDP N-acetylglucosamine transporter mRNA, complete cds	9e-79	3298605	(AF057365) UDP N-acetylglucosamine transporter [Canis familiaris]	9e-10
1466	AJ006064	Rattus norvegicus mRNA for coronin-like protein	1e-82	3757680	(AJ006064) coronin-like protein [Rattus norvegicus]	3e-62
1467	U91582	Macaca fascicularis UDP-glucuronosyltransferase mRNA, complete cds	4e-89	140396	KARYOGAMY PROTEIN KAR4 yeast (Saccharomyces cerevisiae)	1e-08
1468	X06762	Mouse Hox2.3 mRNA	3e-92	123255	HOMEOBOX PROTEIN HOX-B7 (HOX-2C)	9e-23
1469	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	5e-94	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	7e-34
1470	X74504	M.musculus T10 mRNA	7e-97	1711658	SER/THR-RICH PROTEIN T10 IN DGCR REGION >gi\|480900\|pir\|\|S37488 gene T10 protein - mouse	3e-59

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					UBIQUITIN-CONJUGATING	
1471	U13175	Rattus norvegicus clone ubc10a ubiquitin conjugating enzyme (E217kB) mRNA, complete cds.	3e-98	1351345	ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 3) >gi\|1085588\|pir\|\|S53358 ubiquitin conjugating enzyme (E217kB) - rat >gi\|595666 (U13175) ubiquitin conjugating enzyme [Rattus norvegicus] norvegicus] >gi\|1145691 (U39318) UbcH5C [Homo sapiens]	5e-05
1472	S79873	h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	e-119	<NONE>	<NONE>	<NONE>
1473	D13623	Rat mRNA for p34 protein, complete cds	e-112	480379	ribosome-binding protein p34 - rat sp.]	2e-05
1474	AB013357	Mus musculus mRNA for 49 kDa zinc finger protein, complete cds	e-136	4153886	(AB013357) 49 kDa zinc finger protein	5e-08
1475	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-117	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	4e-32
1476	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	e-103	2494312	TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) subunit [Rattus norvegicus]	3e-42

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1477	X73683	R.norvegicus mRNA for histone H3.3	e-117	122075	~~HISTONE H3.3 (H3.3B) (H3.3Q) histone H3.3 - fruit fly~~ (Drosophila melanogaster) histone H3.3B - chicken >gi\|2119023\|pir\|\|S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136) [Oryctolagus cuniculus] >gi\|8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi\|51198 gallus] >gi\|161190 (M17876) histone H3 [Spisula solidissima] >gi\|211853 (M11393) histone 3.3 [Gallus gallus] >gi\|306848 (M11354) H3.3 histone [Homo sapiens] melanogaster] >gi\|963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	1e-45
1478	U32498	Rattus norvegicus rsec8 mRNA, partial cds	e-108	2143962	rsec8 - rat (fragment) >gi\|1019441 (U32498) rsec8 [Rattus norvegicus]	7e-48
1479	U41736	Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	5e-49
1480	AF041338	Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds	e-119	2895578	(AF041338) vacuolar proton pump subunit SFD alpha isoform [Bos taurus]	3e-49
1481	AF064553	Mus musculus NSD1 protein mRNA, complete cds	e-121	3329465	(AF064553) NSD1 protein [Mus musculus]	2e-50
1482	AB000517	Rattus sp. mRNA for CDP-diacylglycerol synthase, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	2e-51
1483	D38517	Mouse mRNA for Dhm1 protein, complete cds	e-118	2137562	mouse Dhm1 protein - mouse musculus]	6e-54

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		M.domesticus MD6			CDC4 repeat unit-containing	
1484	X54352	mRNA	e-139	1085499	protein - mouse	1e-55
1485	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-118	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) >gi\|1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	5e-57
1486	X80169	M.musculus mRNA for 200 kD protein	e-119	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi\|1083553\|pir\|\|A55117 tsg24	9e-58
1487	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-120	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) >gi\|1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	8e-58
1488	U08215	Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.	e-109	473407	(U08215) NST-1 [Mus musculus]	7e-58
1489	D85926	Mouse mRNA for Ray, complete cds	e-110	1944389	(D85926) Ray [Mus musculus]	2e-58
1490	L20427	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-123	457372	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [Rattus norvegicus]	4e-59
1491	X56044	M.musculus mRNA for protein Htf9C	e-121	3183977	(X56044) protein Htf9C [Mus musculus]	1e-60

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROTO-ONCOGENE	
1492	S74774	p59fyn(T)=OKT3-induced calcium influx regulator	e-163	729896	TYROSINE-PROTEIN KINASE FYN (P59-FYN) >gi\|420217\|pir\|\|A44991 protein-tyrosine kinase (EC 2.7.1.112) fyn - mouse	8e-63
1493	U88873	Mus musculus BUB2-like protein 1 (HBLP1) mRNA, complete cds	e-123	4099611	(U88873) BUB2-like protein 1 [Mus musculus]	1e-63
1494	U48852	Cricetulus griseus HT protein mRNA, complete cds.	e-117	1216486	(U48852) HT protein [Cricetulus griseus]	7e-64
1495	AF032667	Rattus norvegicus rexo70 mRNA, complete cds	e-142	2827160	(AF032667) rexo70 [Rattus norvegicus]	5e-66
1496	M62722	Chinese hamster phosphatidylserine decarboxylase mRNA, 3' end.	e-114	118910	PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME >gi\|109423\|pir\|\|A38732 phosphatidylserine decarboxylase (EC 4.1.1.65) - Chinese hamster (fragment)	2e-67
1497	AF072758	Mus musculus fatty acid transport protein 3 mRNA, partial cds	e-130	3335567	(AF072758) fatty acid transport protein 3; FATP3 [Mus musculus]	1e-67
1498	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	e-113	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	2e-69
1499	U57344	Mus musculus homeobox protein Meis3 mRNA, complete cds	e-143	3024124	HOMEOBOX PROTEIN MEIS3	6e-72
1500	U09874	Mus musculus SKD3 mRNA, complete cds.	e-142	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	1e-72
1501	U72194	Mus musculus muskelin mRNA, complete cds	e-148	3493462	(U72194) muskelin [Mus musculus]	2e-74
1502	X80169	M.musculus mRNA for 200 kD protein	e-155	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi\|1083553\|pir\|\|A55117 tsg24	3e-77

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1503	U72194	muskelin mRNA, complete cds	e-154	3493462	(U72194) muskelin [Mus musculus]	2e-78
1504	Y12836	Cricetulus griseus mRNA for Zn finger factor	e-146	3150148	(Y12836) Zn finger factor [Cricetulus griseus]	3e-83